



#10/a

SEQUENCE LISTING

<100> Lowe E., David
<100> Per E., Troy
Kennedy J., Michael

<120> Anti-Bacterial Vaccine Compositions

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<140> 09/545,199

<141> 2000-04-06

<150> 60/153,453

<151> 1999-09-10

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His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys
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Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro
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Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
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Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala
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aat gtc tta gaa gcc gcc atc caa aac cag ata aaa cgc gtc gtc tgt 144
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 Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
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 Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu His Phe Trp
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 Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu Ser Asn Tyr
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 Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile Pro Ala Glu
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Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln Val Phe Asp
 115 120 125
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 145 150 155 160
 His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile
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 Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln Leu Pro Tyr
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Pro Phe Phe Asp Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu
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Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
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Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
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Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
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Ala Val Leu Glu Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn
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Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile							
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Glu Leu Pro Asp Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg							
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Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser							
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Leu Gln Ala Gln Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu							
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His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn							
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Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln							
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Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile							
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Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu							
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Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile							
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Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg
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 Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser Ala Asn Gln Ser
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 Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg
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 Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile
 180 185 190
 His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp
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 Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr
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 Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys
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 Gln Arg Arg Leu Phe His
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 Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr
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 Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu Ile Gly Leu Ser
 65 70 75 80
 Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln
 85 90 95
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 Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly Phe Ser Met Val
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 Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Leu Ala Leu
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 Phe His

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ggc tta ctt gcc ttc atg agc ttt att atg gtt tgg ctt gtg att gaa 2854
Gly Leu Leu Ala Phe Met Ser Phe Ile Met Val Trp Leu Val Ile Glu
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cgc ttt ctt ttc tta agt cgc gtc aac gtg gca tct tat gaa agc ata 2902
Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser Ile
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His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser Thr
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atc ggt tct aat gca cct tat gta ggt ttg ctt ggt acc gtc att ggt 2998
Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile Gly
70 75 80
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Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile Asp
85 90 95
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Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr Ala
100 105 110
gta ggt att tta gtc gcc att cct gca atg gtg tgt tac aac ggt tta 3142
Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly Leu
115 120 125

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 Gly Arg Lys Val Glu Val Asn Arg Leu Lys Trp Phe Ala Leu Asn Glu
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 Lys Lys Ala Lys Gln Gln Ala
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 20 25 30
 Glu Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser
 35 40 45

Ile His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser
 50 55 60
 Thr Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile
 65 70 75 80
 Gly Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile
 85 90 95
 Asp Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
 100 105 110
 Ala Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly
 115 120 125
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 Glu Lys Lys Ala Lys Gln Gln Ala
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 Gln Pro Ala Gln Glu His Cys Gln Arg Ile Asn Asn Ile Val Asn Gln
 5 10 15
 gaa aac ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag 632
 Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu
 20 25 30

cgt tct gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca	680
Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr	
35 40 45	
gtt cat act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg	728
Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val	
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agt tat aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt	776
Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val	
70 75 80	
gcg gta cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg	824
Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu	
85 90 95	
caa gaa caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc	872
Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile	
100 105 110	
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Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser	
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gaa tca aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga	968
Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly	
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aca ttt aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt	1016
Thr Phe Asn Ala Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe	
150 155 160	
aac caa aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg	1064
Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr	
165 170 175	
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Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly	
180 185 190	
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Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu	
195 200 205	
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Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn	
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Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr	
230 235 240	
caa aaa gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc	1304
Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser	
245 250 255	
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Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr	
260 265 270	
gat ttc att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa	1400
Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys	
275 280 285	

cta gaa ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt	1448
Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg	
290 295 300 305	
ggt aag ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta	1496
Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu	
310 315 320	
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Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu	
325 330 335	
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Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro	
340 345 350	
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Asn Leu Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Leu Ser	
355 360 365	
cct att gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa	1688
Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu	
370 375 380 385	
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Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp	
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Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys	
405 410 415	
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Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Arg Gly Asn	
420 425 430	
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Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu	
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ttc ttt gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga	1928
Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly	
450 455 460 465	
gaa gag ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc	1976
Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr	
470 475 480	
aat cta gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga	2024
Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg	
485 490 495	
gaa aaa gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg	2072
Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu	
500 505 510	
cag gag tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa	2120
Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys	
515 520 525	
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Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys	

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cgt gtt gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa	Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys	550		555		560	2216
att gct aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa	Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu	565		570		575	2264
att cgc cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag	Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu	580		585		590	2312
aag aaa caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct	Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala	595		600		605	2360
gaa cag aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac	Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp	610		615		620	2408
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gca tca aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa	Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys	645		650		655	2504
gtg gaa act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa	Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln	660		665		670	2552
gat gac tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat	Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn	675		680		685	2600
aca aaa ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat	Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp	690		695		700	2648
cat caa gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt	His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu	710		715		720	2696
aac caa aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg	Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met	725		730		735	2744
gac aat tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg	Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala	740		745		750	2792
gca tta act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg	Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp	755		760		765	2840
tat gtc aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt	Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val	770		775		780	2888

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Tyr	Phe	Ala	Ser	Glu	Thr	Leu	Val	Glu	Ala	Gln	Lys	Leu	Gln	Gly	Leu	
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ggc	act	ggg	act	atc	aga	gtt	ggt	gaa	gct	aag	att	aaa	gcc	aaa	gat	2984
Gly	Thr	Gly	Thr	Ile	Arg	Val	Gly	Glu	Ala	Lys	Ile	Lys	Ala	Lys	Asp	
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Val	Val	Asn	Thr	Gly	Thr	Leu	Ala	Gly	Arg	Lys	Leu	Asn	Val	Glu	Ala	
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agt	aat	aaa	atc	aaa	aat	caa	ggg	agt	atc	tta	agt	act	caa	gaa	aca	3080
Ser	Asn	Lys	Ile	Lys	Asn	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Gln	Glu	Thr	
	835					840					845					
cgt	tta	gtc	ggg	cgt	aaa	ggg	att	gaa	aac	gta	tct	cgt	tca	ttt	gca	3128
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Asn	Asp	Glu	Leu	Gly	Val	Thr	Ala	Gln	Arg	Ser	Glu	Ile	Lys	Thr	Glu	
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ggt	cat	tta	cat	ctt	gaa	aca	gat	aag	gat	tca	act	att	gat	gta	caa	3224
Gly	His	Leu	His	Leu	Glu	Thr	Asp	Lys	Asp	Ser	Thr	Ile	Asp	Val	Gln	
			885					890					895			
gca	tcg	gat	att	aaa	gca	aaa	aca	agc	ttt	gtg	aag	act	ggt	gat	gtg	3272
Ala	Ser	Asp	Ile	Lys	Ala	Lys	Thr	Ser	Phe	Val	Lys	Thr	Gly	Asp	Val	
		900					905					910				
aat	ctc	aaa	aat	aca	tac	aat	act	aaa	cat	gcc	tac	cgt	gag	aaa	ttc	3320
Asn	Leu	Lys	Asn	Thr	Tyr	Asn	Thr	Lys	His	Ala	Tyr	Arg	Glu	Lys	Phe	
	915					920					925					
tcg	ccg	agt	gca	cta	caa	gtt	gca	gaa	ctt	gat	gtg	gca	ggg	ctt	aaa	3368
Ser	Pro	Ser	Ala	Leu	Gln	Val	Ala	Glu	Leu	Asp	Val	Ala	Gly	Leu	Lys	
930					935					940					945	
gtc	cca	ctt	tta	ggc	gtg	tcg	tct	cca	tcc	agt	tat	tca	gag	cat	act	3416
Val	Pro	Leu	Leu	Gly	Val	Ser	Ser	Pro	Ser	Ser	Tyr	Ser	Glu	His	Thr	
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agt	gag	gca	act	tca	gag	gga	tca	atc	ttc	gaa	gta	ggg	cac	tta	cat	3464
Ser	Glu	Ala	Thr	Ser	Glu	Gly	Ser	Ile	Phe	Glu	Val	Gly	His	Leu	His	
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ctt	gcg	gta	gac	aga	gat	gtg	aac	caa	gcg	ggg	agt	aaa	att	aag	gct	3512
Leu	Ala	Val	Asp	Arg	Asp	Val	Asn	Gln	Ala	Gly	Ser	Lys	Ile	Lys	Ala	
		980					985					990				
aag	tat	acc	act	ggt	gtt	gtg	aaa	ggg	aac	ttt	aat	act	gaa	gcg	ggc	3560
Lys	Tyr	Thr	Thr	Gly	Val	Val	Lys	Gly	Asn	Phe	Asn	Thr	Glu	Ala	Gly	
	995				1000						1005					
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Lys	Asn	Ile	Lys	His	Val	Glu	Lys	Glu	Glu	Tyr	Ser	Ser	Gln	Leu	Phe	
1010				1015						1020					1025	
gct	tca	gca	cac	gcg	agt	ggt	ggt	ggc	acc	tca	gtt	cgt	tat	gac	tat	3656
Ala	Ser	Ala	His	Ala	Ser	Gly	Gly	Gly	Thr	Ser	Val	Arg	Tyr	Asp	Tyr	

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aac agc caa gat ggt ggc aat gcc tct gtt ggt gtt ccg aca aac cat	3704														
Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn His															
1045	1050	1055													
act gga gtt ggg gca gag gca gga atg tca ttc acc cat acc aaa gac	3752														
Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys Asp															
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aaa gaa aca ctg ctc act cac acc aat agt gaa tta caa gtc aaa cat	3800														
Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys His															
1075	1080	1085													
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Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp Ile															
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aat act aaa cta cca gaa gat gca caa agc aaa gca cag aaa gag ata	3896														
Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu Ile															
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gcg gct agc aag cca gag aag acc gag caa tct gca cag gat gtg gct	3944														
Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val Ala															
1125	1130	1135													
caa gct caa tca aat gcc aat aag gat aag gaa aat aaa gcc cca gaa	3992														
Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro Glu															
1140	1145	1150													
ata aaa gaa tta tca gag gct gaa atc gcg gat ctc atg tca gaa aaa	4040														
Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu Lys															
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tca aaa gcg tat ttt gat gat ttt gca gag caa gcg aaa aaa gca cct	4088														
Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala Pro															
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Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser Lys															
1190	1195	1200													
caa aaa gac caa tat gat cat gag tct gaa cgg acg act ttt aaa gtt	4184														
Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys Val															
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Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser His															
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Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp Gly															
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aca gta gca tta caa cat gct agt gat gtc tta aat att gtg acg ggg	4328														
Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr Gly															
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Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His Glu															
1270	1275	1280													

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1285 1290 1295	
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1300 1305 1310	
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aat gtg ctg tct ggt gaa aaa aca cga gaa acc aca gaa aca gta tca Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val Ser	4568
1330 1335 1340 1345	
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1350 1355 1360	
ggc gcc tgt act gcc ggt gtt agc aca tca ctt gaa gga aat gaa agc Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu Ser	4664
1365 1370 1375	
tat acg tca gaa cgt gaa acg gct caa aat aac agt ttc tta aaa gca Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys Ala	4712
1380 1385 1390	
cgc aac atg aaa gtt gaa gca ggt cgc gat ttt aat gtt gtc agt tcg Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser Ser	4760
1395 1400 1405	
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gtg gta tcc aaa caa gat acg tta caa aaa gtg acg cat gga gtt gac Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val Asp	4856
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cca acc ggt aat gtt ggt ttc ggt tat acc aat gag acc gaa agc aag Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser Lys	4952
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Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg Ala															
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Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu Thr															
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Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln Phe															
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Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro Ile															
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tca gag cat att tat act gat att agc gac gtg ggc act caa act aaa Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr Lys 1795 1800 1805	5960
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aac gat ggt tgg gtt gaa gta gaa aaa cat acc ttg cgt cac cgt cgt Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg Arg 1990 1995 2000	6536
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2020	2025	2030	
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gcg cca tta gaa gaa ctg tgg gca aca tgg gca att aaa aca tta ggt Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu Gly 2085 2090 2095			6824
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tga			6876
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Gln Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala 20 25 30			
Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu 35 40 45			
Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn 50 55 60			
Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg 65 70 75 80			
Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn 85 90 95			
Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala 100 105 110			
Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser 115 120 125			
Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys 130 135 140			
Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala 145 150 155 160			
Phe Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile			

165							170					175				
Thr	Met	Tyr	Tyr	Gln	Pro	Leu	Thr	Arg	Tyr	Ile	Trp	Thr	Pro	Leu	Ser	
			180					185					190			
Gly	Asn	Ala	Ser	Arg	Glu	Phe	Asn	Asn	Leu	Glu	Ser	Phe	Leu	Asp	Ala	
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Leu	Phe	Gly	Ser	Thr	Thr	Ile	Leu	Lys	Ser	Ser	Phe	Tyr	Ser	Thr	Glu	
	210					215					220					
Asn	Phe	Ser	Ala	Tyr	Gln	Leu	Leu	Ser	His	Ile	Gln	His	Ser	Pro	Met	
225					230					235				240		
Tyr	Gln	Lys	Ala	Met	Ala	Gln	Val	Phe	Gly	Ala	Glu	Trp	His	Ser	Lys	
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Ser	Tyr	Asp	Glu	Met	Arg	Asn	Lys	Trp	Lys	Ser	Phe	Lys	Glu	Asn	Pro	
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Thr	Asp	Phe	Ile	Tyr	Tyr	Pro	Ser	Glu	Lys	Ala	Lys	Ile	Leu	Ala	Gly	
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Lys	Leu	Glu	Gly	Lys	Leu	Thr	Thr	Leu	Gln	Asn	Gly	Glu	Tyr	Ala	Glu	
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Arg	Gly	Lys	Phe	Asp	Glu	Ser	Ile	Gln	Ile	Gly	Lys	His	Gln	Leu	Ser	
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Glu	Glu	Asp	Gly	Val	Asp	Leu	Ser	Ser	Ile	Ala	Glu	Leu	Leu	Glu	Met	
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Pro	Asn	Leu	Phe	Ile	Asp	Asn	Ser	Ile	Gln	Leu	Glu	Lys	Lys	Lys	Leu	
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	370					375					380					
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385					390					395					400	
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Lys	Glu	Met	Pro	Asp	Asp	Lys	Leu	Gly	Ile	Ser	Arg	Asp	Asp	Arg	Gly	
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Asn	Lys	Pro	Pro	Arg	Thr	Asp	Pro	Thr	Val	Asp	Tyr	Leu	Asn	Pro	Asp	
		435					440					445				
Glu	Phe	Phe	Glu	Asn	Gly	Tyr	Leu	Leu	Asn	Glu	Leu	Leu	Gln	Glu	Leu	
	450					455					460					
Gly	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Gly	Glu	Asp	His	Phe	Lys	Arg	Ser	
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Thr	Asn	Leu	Val	Arg	Leu	Gly	Glu	Arg	Asp	Arg	Gln	Asn	Arg	Glu	Lys	
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Arg Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys
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 Leu Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln
 515 520 525
 Lys Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu
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 545 550 555 560
 Lys Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu
 565 570 575
 Glu Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu
 580 585 590
 Glu Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln
 595 600 605
 Ala Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu
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 Asp Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala
 625 630 635 640
 Glu Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro
 645 650 655
 Lys Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn
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 Gln Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu
 675 680 685
 Asn Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe
 690 695 700
 Asp His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His
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 Leu Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu
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 Met Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly
 740 745 750
 Ala Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val
 755 760 765
 Trp Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys
 770 775 780
 Val Tyr Phe Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly
 785 790 795 800
 Leu Gly Thr Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys
 805 810 815
 Asp Val Val Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu
 820 825 830

Ala Ser Asn Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu
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 Thr Arg Leu Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe
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 Gln Ala Ser Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp
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 Val Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys
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 Phe Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu
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 Lys Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His
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 Thr Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu
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 His Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys
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 Ala Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala
 995 1000 1005
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 Asp Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys
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 Pro Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser
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 Lys Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys
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 Val Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser
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 His Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp
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 Gly Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr
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 Gly Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn
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 2005 2010 2015
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Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu Thr Glu Gly Asn Asn Phe	570	575	580	
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Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys	85	90	95	
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Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu	165	170	175	
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Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val	195	200	205	
Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn	210	215	220	

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Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
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Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
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Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
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Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys	
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Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln	
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gagcttatag atccgaatca gatgatgtta aagggttaca aaggaaatgt gatcattgat			2276
attgatgggt tttcgacaga tggattaaag tatttagata ttattgctaa aaaaattgaa			2336
caaaagcaat caattacatc aggggataat tcagaagcaa aaacagatgt cactcttatt			2396
gcgggttcca gtgaatatga tttaagcaaa catgagctga aaaaaacgag cggtgaaaat			2456
gtatctaatt atgttattgc tatcacggga tctagtacag gcgcaatgca tggtaaaaat			2516
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gaaaatgata ttcagattga aatgaatgaa ggtgacttag aacttggcaa tacgattcag			2636
caaacagtgg taaaaaaaga ccgaaatatt cgagccaaga aaaaattga agtgaaaaac			2696
gctaatacgtg tttttgttgg tagtcaaacg aaatcagatg aaatttcgtt agaggcgaaa			2756
caagttaaaa tcagaaaaaa cgcagagatt aggagtacga cacaagccaa aatcgtagca			2816
aagggtgccc tgtctattga gcaaaatgcg aagctcgtcg ctaaaaagat agatgtggca			2876

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<212> PRT
<213> Pasteurella multocida

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Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
35 40 45
Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe
50 55 60
Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys
65 70 75 80
Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
85 90 95
Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
100 105 110
Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu
115 120 125
Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe
130 135 140
Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala
145 150 155 160
Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu
165 170 175
Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys
180 185 190
Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln
195 200 205
Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr
210 215 220

Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr
 225 230 235 240
 Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu
 245 250 255
 Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser
 260 265 270
 Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser
 275 280 285
 Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser
 290 295 300
 Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser
 305 310 315 320
 Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser
 325 330 335
 Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr
 340 345 350
 Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
 355 360 365
 Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
 370 375 380
 Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
 385 390 395 400
 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
 405 410 415
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
 420 425 430
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
 435 440 445
 Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
 450 455 460
 Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
 465 470 475 480
 Ser Phe

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 <212> DNA
 <213> Pasteurella multocida

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 <222> (639)..(1022)

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 <223> greA

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gtacgataag atcgccatgc atttcattgt tttttatttt tccattgggt aatagactgg 180
tttcaaattg aaattgggtca cttagtacga gtttggcggt taaggcgggtg agcacttttt 240
gtgtactggc gggtaacata aagggtactgg cttgggtgcgc tacaattttt tcattacgat 300
ttaagttttt agccacaaaa cctaggctgg tcccttcggg taaatgagcg ttgatttcag 360
caagatcaat ctcagcataa ctgaaatgac tgacgagtaa actacatata agtatcggtc 420
gtttgaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tattttatac ataattggct 480
cgagcagttg ctattttttt attgtcgaac aataatagta tttgaaccct cgagagtaaa 540
tcctttttctc gttaaacact tattttttta ttcaactacg gcattgtttt tacaatgttg 600
tggttttggt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656
                                     Met Lys Gln Ile Pro Met
                                     1           5

act ata cgt ggt gcg gaa caa tta aga caa gaa ctc gat ttt ttg aaa 704
Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln Glu Leu Asp Phe Leu Lys
                10                15                20

aac act cgt cgc cca gaa att att aat gct atc gca gaa gct cgt gaa 752
Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu
                25                30                35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag 800
His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln
                40                45                50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg 848
Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu Ile Glu Gly Lys Leu Ala
                55                60                65                70

aat agt caa att att gat gtc aca aag atc cca aat aat ggc aaa gtg 896
Asn Ser Gln Ile Ile Asp Val Thr Lys Ile Pro Asn Asn Gly Lys Val
                75                80                85

att ttt ggt gcc aca att ttg tta ctg aat att gac acg gaa gaa gaa 944
Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn Ile Asp Thr Glu Glu Glu
                90                95                100

gtc tcg tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg 992
Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly
                105                110                115

cta att tca gtt aac gcc acg cga ttg aat tagagaaagc taaatggatt 1042
Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
                120                125

gcccaagatc ttggcggtcaa acaaacgtta attgacactt ccgtcattaa agcgattacg 1102
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<210> 22
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 <213> Pasteurella multocida

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 Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr
 35 40 45
 His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu
 50 55 60
 Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile
 65 70 75 80
 Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
 85 90 95
 Ile Asp Thr Glu Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
 100 105 110
 Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
 115 120 125

<210> 23
 <211> 4666
 <212> DNA
 <213> Pasteurella multocida

<220>
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 <222> (980)..(2440)

<220>
 <223> guaB

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 gcgatcaatt tattccgata aatcgttggt aatacttcaa tcagctctgc ccaagggtga 180
 tcaatttgct gtgtttgttt tgggaaagac aaattaatgc caaagccaat cacgagatta 240
 tgttgattat tctgacgatt ggcgatttcg accaaaatcc ctgctaattt gcgcccattg 300
 aatagcacat catttggcc ttttaatcca atgttcaaag cacctgcttg ctttagcggt 360
 tctgcgattg ccataccac tactaaactc aagccttcta aattgacctt ttggtcacat 420
 gcccaataca aactcataat cacttggtcca gcaaaaggag aaagccattg acgaccacgt 480
 cgtccacgtc ccgcagtttg atattctgct aagcaaatag cgcttttttc caaatgtgca 540
 atattgtcaa gcaagaattg attggtcgag ttaataatcg gcttaatata aagtgggtaa 600

ggcgtaacg	cttgctcaa	ataagattca	tttaagcgac	ttaattgagg	tatgagacga	660
aaatgttgga	cttgctgttc	tatttgatc	ccttggtgtt	tcaatttttc	gatattgtgt	720
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aggcaactta	ttatagacaa	tgatttttctc	gaaaatcgat	aaaaaaatcc	attttcaaac	900
agcaacgaaa	tctgtataat	gcgaccgcaa	tatttttttac	cctttttat	ttcatatcaa	960
cctaagagag	aatattgca	atg tta cga gta ata	aaa gaa gca tta	acc ttc		1012
		Met Leu Arg Val Ile	Lys Glu Ala Leu	Thr Phe		
		1	5	10		
gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc						1060
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr						
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gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca						1108
Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro						
	30		35		40	
atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc						1156
Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile						
	45		50		55	
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct						1204
Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser						
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att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc						1252
Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser						
	80		85		90	
ggt att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca						1300
Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala						
	95		100		105	
gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt						1348
Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val						
	110		115		120	
gtt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca						1396
Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr						
	125		130		135	
cgc ttt gtc acg gat tta aat aaa aca gtg gcg gac ttt atg acc cct						1444
Arg Phe Val Thr Asp Leu Asn Lys Lys Thr Val Ala Asp Phe Met Thr Pro						
	140		145		150	155
aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att						1492
Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile						
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Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser						
	175		180		185	
gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa						1588
Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys						
	190		195		200	

tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg 205 210 215	1636
gtc ggt gct gca gta gga gca gga cct ggt aat gaa gaa cgt att gat Val Gly Ala Ala Val Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp 220 225 230 235	1684
gca tta gtg aaa gca ggg gtc gat gtg tta ttg att gac tca tca cac Ala Leu Val Lys Ala Gly Val Asp Val Leu Leu Ile Asp Ser Ser His 240 245 250	1732
ggt cat tca gaa ggt gtg tta caa cgt gtg cgt gaa act cgt gcg aaa Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys 255 260 265	1780
tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly 270 275 280	1828
gca att gcg ttg gct gat gca ggg gca agt gca gtg aaa gtg ggg att Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile 285 290 295	1876
ggt cct ggt tca att tgt aca aca cgt att gtc aca ggc gtg ggc gtt Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val 300 305 310 315	1924
cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg 320 325 330	1972
ggt att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile 335 340 345	2020
tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg Ser Lys Ala Ile Ala Ala Gly Ala Ser Cys Val Met Val Gly Ser Met 350 355 360	2068
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cgt gcc ttt aaa tct tat cga ggt atg gga tcg tta ggt gcg atg agc Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser 380 385 390 395	2164
aaa ggc tca agc gac cgc tat ttc cag tcc gat aat gca gct gac aaa Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys 400 405 410	2212
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aaa gaa att atc cat caa caa atg ggt gga ttg cgt tct tgt atg ggc Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly 430 435 440	2308
tta acg ggt tgt gca acc att gat gaa ctc cgt acc aaa gcg cag ttt Leu Thr Gly Cys Ala Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe 445 450 455	2356

445	450	455	
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Val Arg Ile Ser Gly Ala Gly Ile Gln Glu Ser His Val His Asp Val			
460	465	470	475
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Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly			
480	485		
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<210> 24

<211> 487

<212> PRT

<213> Pasteurella multocida

<400> 24

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Val	Pro	Ala	His	Ser	Thr	Val	Leu	Pro	Asn	Thr	Ala	Asp	Leu	Ser	Thr	20	25	30	
Gln	Leu	Thr	Lys	Thr	Ile	Arg	Leu	Asn	Ile	Pro	Met	Leu	Ser	Ala	Ala	35	40	45	
Met	Asp	Thr	Val	Thr	Glu	Thr	Lys	Leu	Ala	Ile	Ser	Leu	Ala	Gln	Glu	50	55	60	
Gly	Gly	Ile	Gly	Phe	Ile	His	Lys	Asn	Met	Ser	Ile	Glu	Arg	Gln	Ala	65	70	75	80
Glu	Arg	Val	Arg	Lys	Val	Lys	Lys	Phe	Glu	Ser	Gly	Ile	Val	Ser	Asp	85	90	95	
Pro	Val	Thr	Val	Ser	Pro	Thr	Leu	Ser	Leu	Ala	Glu	Leu	Ser	Glu	Leu	100	105	110	
Val	Lys	Lys	Asn	Gly	Phe	Ala	Ser	Phe	Pro	Val	Val	Asp	Asp	Glu	Lys	115	120	125	
Asn	Leu	Val	Gly	Ile	Ile	Thr	Gly	Arg	Asp	Thr	Arg	Phe	Val	Thr	Asp	130	135	140	
Leu	Asn	Lys	Thr	Val	Ala	Asp	Phe	Met	Thr	Pro	Lys	Ala	Arg	Leu	Val	145	150	155	160
Thr	Val	Lys	Arg	Asn	Ala	Ser	Arg	Asp	Glu	Ile	Phe	Gly	Leu	Met	His	165	170	175	
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Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
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 Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
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 Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
 225 230 235 240
 Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
 245 250 255
 Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
 260 265 270
 Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
 275 280 285
 Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
 290 295 300
 Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
 305 310 315 320
 Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile
 325 330 335
 Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala
 340 345 350
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
 355 360 365
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
 370 375 380
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
 385 390 395 400
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
 405 410 415
 Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His
 420 425 430
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
 435 440 445
 Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
 450 455 460
 Ala Gly Ile Gln Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
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 Ala Pro Asn Tyr Arg Met Gly
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<210> 25
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 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (191)..(1828)

<220>
 <223> H11501

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 Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala
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 caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg 421
 Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly
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 Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp
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Glu	Asn 415	Glu	Thr	Ile	Leu	Ser 420	Ala	Val	Gln	His	Asp 425	Phe	Lys	Thr	Asp	
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 Ser Ala Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly
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 Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp
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gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac 1765
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Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala Gln His Glu

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Glu	Leu	Phe 115	Tyr	Gln	Phe	Pro	Met 120	Leu	Glu	Asp	Leu	Met 125	Val	Asp	Met
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Pro	Phe	Gly	Ala	Thr 245	Asn	Asp	Glu	Lys	Arg 250	Thr	Leu	Leu	Arg	Ala 255	Leu
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Pro	Tyr 355	Leu	Gln	Ile	Asn	Ile	Asp 360	Pro	Asn	Ile	Leu	Pro 365	Ser	Arg	Val
Pro 370	Tyr	Phe	Glu	Phe	Asp	Thr 375	Lys	Glu	Tyr	Ala	Asp 380	Leu	Ser	Val	Leu

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 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp
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 Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val
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 Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn
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 485 490 495
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Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
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ggg ctt agt gat gca gtg cgt ttt gct aat gat caa acc cct tat ctc 145
Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
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cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
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gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
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caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg 289
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
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ttt gta tat tta caa aga cag aat ata gct cgg gga gaa ttt tca acg 337
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
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agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc 385
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
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gaa ttt cgt gat ang ttt tta gaa aat atg aat aag cnt ttt acg ttt 433
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
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cgg ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat 481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
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aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg 529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
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gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg 577
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg
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tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc 625
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Gly	Trp	Ser	Val	Ser	Leu	Ser	Gly	Arg	Tyr	Ser	Ala	Ala	Lys	Lys	Ala	
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Lys	Asp	Ala	Ile	Glu	Thr	Glu	Tyr	Thr	His	Asp	Lys	Lys	Val	Val	Lys	
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Gln	Trp	Pro	His	Leu	Ser	Pro	Ser	Tyr	Phe	Val	Val	Asp	Phe	Thr	Gly	
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 Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
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 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
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 Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
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 Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
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 Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
 115 120 125
 Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
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 Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
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 Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile

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			260					265					270																
Thr	Tyr	Leu	Gln	His	Ser	Arg	Gly	His	Asp	Leu	Ser	Tyr	Asn	Leu	Val														
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Cys	Asp	Ser	Tyr	Lys	Asn	Pro	Leu	Gly	Leu	Gln	Phe	Lys	Asp	Gly	Gln														
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Ile	Leu	Asp	Pro	Ala	Gly	Asn	Lys	Ile	Lys	Leu	Gln	Gly	Ser	Gly	Leu														
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Ser	Thr	Gln	Ile	Val	Asp	Glu	Asn	Gly	Lys	Pro	Phe	Pro	Thr	Thr	Thr														
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Gly Phe Trp Leu Asp Cys Ser Val Phe Asp Cys Asn Lys Pro Phe Thr
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 Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln Ala Arg Glu Val Leu Leu
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 Ser Glu Glu Ile Thr Val Asp Gly Lys Leu Tyr Lys Thr Ala Lys Glu
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 Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr
 465 470 475 480
 Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu Asn Thr Asn Thr Lys Gln
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 Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn
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 Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg Ile Glu Lys Glu Met Ile
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 Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro Thr Trp Trp Ala Asp Arg
 530 535 540
 Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr Asn Ala Leu Lys Cys Pro
 545 550 555 560
 Lys His Glu Pro Leu Thr Ser Phe Leu Ile Pro Val Glu Ala Thr Thr
 565 570 575
 Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser
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 Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr
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 Thr Pro Gly Val Thr Pro Lys Ile Pro Asp Asp Met Val Lys Gly Leu
 610 615 620
 Phe Ile Pro Met Pro Lys Glu Pro Gln Leu Lys Asp Phe Asp Tyr Asn
 625 630 635 640
 Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro
 645 650 655
 Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile Ala Gln Asp Lys Thr Phe
 660 665 670
 Lys Lys His Ser Tyr Ser Leu Gly Ala Thr Phe Asp Pro Leu Asn Phe
 675 680 685
 Leu Arg Val Gln Val Lys Tyr Ser Lys Gly Phe Arg Ala Pro Thr Ser
 690 695 700
 Asp Glu Leu Tyr Phe Thr Phe Lys His Pro Asp Phe Thr Ile Leu Pro
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 Asn Pro Val Leu Lys Pro Glu Glu Ala Lys Asn Gln Glu Ile Ala Leu
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 Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr
 740 745 750

Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu
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 Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr
 770 775 780
 Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn
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 Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn
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 Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly Arg Leu Asp Gly Asp Arg
 820 825 830
 Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr
 835 840 845
 Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val
 850 855 860
 Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln
 865 870 875 880
 Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu
 885 890 895
 Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln
 900 905 910
 Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser
 915 920 925
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 Leu Ser Ala Glu Ile Thr Phe
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<213> Pasteurella multocida

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<222> (1106)..(1564)

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ttcttcgtca gggcgatcaa tataaggggg caatggcata tgcccaattt gctgtaacac 180

gtctaaaagt	gcggtctgtt	tttgcgcgat	ttctaattca	aataaggtat	catggcgcg	240										
aaccatgac	attttgacac	catgatgttc	acctaactta	tcttcgccta	accacagttc	300										
tgccccctt	ttcggtgctt	ttgaggagcg	cacatgggct	aaaaagcgtg	tgtcggataa	360										
aatccgctcg	accaacactt	ccaccttacc	gccactggct	ttacgtccaa	acatccttgc	420										
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gagatgattt	tggacaaaaa	aaaagccctt	tcaagaaaga	cgaaagggcg	aaaatatatt	780										
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ccgttaaata	accaagaggt	ggaag	atg	aca	gaa	gaa	aat	aaa	gga	aag	aga	1132				
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tat	ttt	tta	tgg	ttc	ata	ttg	ttt	atc	ctt	tca	atc	tat	tta	ttt	att	1180
Tyr	Phe	Leu	Trp	Phe	Ile	Leu	Phe	Ile	Leu	Ser	Ile	Tyr	Leu	Phe	Ile	
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acc	ata	caa	gaa	aga	cga	ggt	tat	tgt	ttt	gac	aaa	cgt	gca	tat	att	1228
Thr	Ile	Gln	Glu	Arg	Arg	Gly	Tyr	Cys	Phe	Asp	Lys	Arg	Ala	Tyr	Ile	
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cat	gag	ctt	tat	act	gag	caa	gag	tta	att	gat	cgg	ggg	att	gaa	tat	1276
His	Glu	Leu	Tyr	Thr	Glu	Gln	Glu	Leu	Ile	Asp	Arg	Gly	Ile	Glu	Tyr	
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gtg	gta	tcc	acc	atg	ccg	tca	ggt	ggt	att	aaa	cca	gat	ggc	aca	ata	1324
Val	Val	Ser	Thr	Met	Pro	Ser	Gly	Val	Ile	Lys	Pro	Asp	Gly	Thr	Ile	
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aaa	gaa	gta	aag	cgt	tac	acg	agt	gtc	gag	gag	ttt	aaa	cag	atg	aac	1372
Lys	Glu	Val	Lys	Arg	Tyr	Thr	Ser	Val	Glu	Glu	Phe	Lys	Gln	Met	Asn	
	75					80					85					
cca	gct	tgt	tgt	aca	tta	acc	acc	ttt	att	gat	gaa	gga	ggc	gat	ggc	1420
Pro	Ala	Cys	Cys	Thr	Leu	Thr	Thr	Phe	Ile	Asp	Glu	Gly	Gly	Asp	Gly	
	90				95					100					105	
tat	cca	gat	gat	gat	gga	tat	ggt	tat	gtc	aga	att	gaa	tat	tta	aga	1468
Tyr	Pro	Asp	Asp	Asp	Gly	Tyr	Gly	Tyr	Val	Arg	Ile	Glu	Tyr	Leu	Arg	
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cat	tat	gtt	gag	aat	cta	aaa	cct	tat	cat	aga	gtg	att	tat	ctt	gaa	1516

His	Tyr	Val	Glu	Asn	Leu	Lys	Pro	Tyr	His	Arg	Val	Ile	Tyr	Leu	Glu	
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ctgattgttg	taaattaaca	agatttatta	atgaaggaat	agatggctat	ccagatgatg	2044	
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cggcaacatt	gtgaatgtgg	gtgaagaaat	tccagtgaag	aatgtagcac	cgacacttgg	2944	
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Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln	35	40	45
Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser	50	55	60
Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr	65	70	75
Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr	85	90	95
Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr	100	105	110
Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys	115	120	125
Pro Tyr His Arg Val Ile Tyr Leu Glu Tyr Thr Pro Cys Gly Glu Leu	130	135	140
Arg Glu Glu Ala Ala Phe Ser Lys Asn	145	150	

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110 115 120	
aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag	735
Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys	
125 130 135	
tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt	783
Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe	
140 145 150	
aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat	831
Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp	
155 160 165	
gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg	879
Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Gln Met	
170 175 180 185	
att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc	927
Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val	
190 195 200	
tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga	975
Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg	
205 210 215	
ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa	1023
Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu	
220 225 230	
aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa	1071
Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys	
235 240 245	
gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa	1119
Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys	
250 255 260 265	
ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct	1167
Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser	
270 275 280	
ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc	1215
Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe	
285 290 295	
aaa tat caa gtc tat taactattga atttttgcaa atgagataag agtatagtgc	1270
Lys Tyr Gln Val Tyr	
300	
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tattcatctt gattttgaag gaaagagagt gttttttgta taaaagcatt ttcgtcacct	1390
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tccatggata ttacaggtgt accgcaagcc atgctttcta ggataactgt cggtaacccc	1510
tctttcaaag aggtgtgtaa aaatagctta gcatttttta ttaatggata cggattatct	1570
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1683

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 35 40 45
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
 85 90 95
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
 100 105 110
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
 115 120 125
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
 130 135 140
 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe

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Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile						
	180		185			190
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe						
	195		200			205
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly						
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Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val						
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Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys						
	245		250			255
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg						
	260		265			270
Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala						
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Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr						
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gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97
 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
 20 25 30

nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
 35 40 45

tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193
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 50 55 60

tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
 65 70 75 80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
 85 90 95

atc ttc ngg gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
 100 105 110

ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385
 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
 115 120 125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433
 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
 130 135 140

gaa ggc aca aaa tgg cag tta aaa cga tcg tgt cct acg tat ccc tta 481

Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
 145 150 155 160

tgt tgg tgt gga tgc gga taacttaaag gagttcctaa aataataaac 529
 Cys Trp Cys Gly Cys Gly
 165

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<211> 166

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<213> Pasteurella multocida

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 35 40 45
 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
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 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
 65 70 75 80
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 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
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 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
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Ile Leu Glu Gln Gln Asp Tyr Pro Val Arg Leu Glu His Gly Pro Asn
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Phe Glu Glu Val Ile Asp Glu Lys Cys Trp Leu Val Val Thr Ser Thr
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cat ggt gca ggt gaa tta ccg gat aat att aaa cct ctg ttt gaa aaa 544
His Gly Ala Gly Glu Leu Pro Asp Asn Ile Lys Pro Leu Phe Glu Lys
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tta gca ttt cac cca aaa cag tta gct gac tta cgc ttt gcg gtg atc 592
Leu Ala Phe His Pro Lys Gln Leu Ala Asp Leu Arg Phe Ala Val Ile
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Gly Leu Gly Asn Ser Asp Tyr Asp Thr Phe Cys His Ala Val Asp His
90                               95                               100                               105

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Val Glu Gln Leu Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser
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cta aga atg gat atg cta acc att act gat cct gaa cac acg gcc gaa 736
Leu Arg Met Asp Met Leu Thr Ile Thr Asp Pro Glu His Thr Ala Glu
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<212> PRT

<213> Pasteurella multocida

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 Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
 35 40 45
 Lys Cys Trp Leu Val Val Thr Ser Thr His Gly Ala Gly Glu Leu Pro
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 Asp Asn Ile Lys Pro Leu Phe Glu Lys Leu Ala Phe His Pro Lys Gln
 65 70 75 80
 Leu Ala Asp Leu Arg Phe Ala Val Ile Gly Leu Gly Asn Ser Asp Tyr
 85 90 95
 Asp Thr Phe Cys His Ala Val Asp His Val Glu Gln Leu Leu Leu Ser
 100 105 110
 Lys Asp Ala Leu Gln Leu Cys Glu Ser Leu Arg Met Asp Met Leu Thr
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 Ser Gln Leu
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<211> 351

<212> PRT

<213> Pasteurella multocida

<400> 42

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Val	Leu	Asp	Glu	Pro	Ser	Val	Val	Ala	Ile	Arg	Gln	Glu	Arg	Ser	Gly	35	40	45	
Ala	Leu	Lys	Ser	Ile	Ala	Ala	Val	Gly	Arg	Asp	Ala	Lys	Leu	Met	Leu	50	55	60	
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Lys	Gln	Val	His	Ser	Ser	Asn	Phe	Met	Arg	Pro	Ser	Pro	Arg	Val	Leu	100	105	110	
Val	Cys	Val	Pro	Ala	Gly	Ala	Thr	Gln	Val	Glu	Arg	Arg	Ala	Ile	Lys	115	120	125	
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Ile	Ser	Leu	Asn	Gly	Ile	Val	Tyr	Ser	Ser	Ser	Val	Arg	Ile	Gly	Gly	180	185	190	
Asp	Arg	Phe	Asp	Glu	Ala	Ile	Ile	Ser	Tyr	Val	Arg	Lys	Thr	Phe	Gly	195	200	205	
Ser	Ile	Ile	Gly	Glu	Pro	Thr	Ala	Glu	Arg	Ile	Lys	Gln	Glu	Ile	Gly				

210	215	220
Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His		
225	230	235 240
Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser		
	245	250 255
Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala		
	260	265 270
Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp		
	275	280 285
Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg		
	290	295 300
Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile		
305	310	315 320
Ala Asp Asp Pro Leu Thr Cys Val Ala Arg Gly Gly Gly Glu Ala Leu		
	325	330 335
Glu Met Ile Asp Met His Gly Gly Asp Ile Phe Ser Asp Asp Ile		
	340	345 350

<210> 43
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 <212> DNA
 <213> Pasteurella multocida

<220>
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<220>
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1 5 10 15	
gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc gaa gca tac cgt	96
Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg	
20 25 30	
atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct	144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala	
35 40 45	
gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc	192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile	
50 55 60	
agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc	240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile	
65 70 75 80	
gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca	288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr	
85 90 95	

gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt	336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg	
100 105 110	
aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct	384
Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala	
115 120 125	
gtc gcg aca tta ggt aca gaa cgt gat gca caa att att gat gaa tta	432
Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu	
130 135 140	
aca ggt gag cgt tca gat cac ttc tta ttc cac tac aac ttc ccg cca	480
Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro	
145 150 155 160	
tat tct gtg ggt gaa acc ggt atg att ggt tca cca aaa cgt cgt gaa	528
Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu	
165 170 175	
att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct gca gtg atg cca	576
Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro	
180 185 190	
aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc tct gaa atc aca	624
Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr	
195 200 205	
gaa tca aat ggt tct tct tct atg gca tgc gtt tgt ggt gcg tct tta	672
Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu	
210 215 220	
gca tta atg gat gcg ggt gta cca att aaa gcg gcg gtt gca ggt att	720
Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile	
225 230 235 240	
gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg gtg ctt tca gac	768
Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp	
245 250 255	
atc tta ggt gat gaa gat cac tta ggt gac atg gac ttc aaa gtc gcg	816
Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala	
260 265 270	
ggt aca cgt acg ggt gtg acg gca tta caa atg gat atc aaa atc gaa	864
Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu	
275 280 285	
ggt atc aca gca gaa atc atg caa att gcg tta aac caa gcg aaa agc	912
Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser	
290 295 300	
gca cgt tta cac att tta ggt gtg atg gag caa gcg atc cca gcg cca	960
Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro	
305 310 315 320	
cgt gcg gat att tct gat ttt gca ccg cgt att tac act atg aaa att	1008
Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile	
325 330 335	
gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt ggt gca acc att	1056
Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile	

340										345					350					
cgt	gcc	tta	aca	gaa	gaa	aca	ggt	acc	tca	att	gat	atc	gat	gat	gat	1104				
Arg	Ala	Leu	Thr	Glu	Glu	Thr	Gly	Thr	Ser	Ile	Asp	Ile	Asp	Asp	Asp					
355				360				365												
ggt	acg	gtg	aag	att	gct	gcg	ggt	gat	ggc	aat	tca	gca	aaa	gag	gtg	1152				
Gly	Thr	Val	Lys	Ile	Ala	Ala	Val	Asp	Gly	Asn	Ser	Ala	Lys	Glu	Val					
370		375				380														
atg	gcg	cgt	att	gaa	gat	att	act	gca	gaa	gtt	gaa	gcg	ggt	gca	gtg	1200				
Met	Ala	Arg	Ile	Glu	Asp	Ile	Thr	Ala	Glu	Val	Glu	Ala	Gly	Ala	Val					
385		390				395				400										
tat	aaa	ggt	aaa	gtt	act	cgt	tta	gct	gat	ttt	ggt	gcc	ttc	gtt	tct	1248				
Tyr	Lys	Gly	Lys	Val	Thr	Arg	Leu	Ala	Asp	Phe	Gly	Ala	Phe	Val	Ser					
405				410				415												
atc	gta	ggt	aac	aaa	gaa	ggc	tta	gtg	cat	att	tct	caa	atc	gcg	gaa	1296				
Ile	Val	Gly	Asn	Lys	Glu	Gly	Leu	Val	His	Ile	Ser	Gln	Ile	Ala	Glu					
420			425				430													
gag	cgt	gtt	gag	aaa	gtg	agt	gat	tat	ctt	gca	gtg	ggg	caa	gaa	gtg	1344				
Glu	Arg	Val	Glu	Lys	Val	Ser	Asp	Tyr	Leu	Ala	Val	Gly	Gln	Glu	Val					
435		440				445														
act	gtt	aaa	gtg	gtt	gag	att	gat	cgt	caa	ggt	cgt	att	cgt	tta	acc	1392				
Thr	Val	Lys	Val	Val	Glu	Ile	Asp	Arg	Gln	Gly	Arg	Ile	Arg	Leu	Thr					
450		455				460														
atg	aaa	gaa	gtt	gca	cca	aag	caa	gaa	cac	gtt	gat	tct	gtt	gtc	gca	1440				
Met	Lys	Glu	Val	Ala	Pro	Lys	Gln	Glu	His	Val	Asp	Ser	Val	Val	Ala					
465		470				475				480										
gac	gtt	gcc	gca	gaa	gaa	aac	gca	taagcaataa	acaccaacgc	ccttcgtgat	1494									
Asp	Val	Ala	Ala	Glu	Asn	Ala														
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cattcctaaa tagaggggta aattttttatt acgtcggacg ttatgaatta gctcagcggg 2034																				
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<210> 44
 <211> 488
 <212> PRT
 <213> Pasteurella multocida

<400> 44

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			20					25					30		
Ile	Thr	Glu	Asn	Lys	His	Val	Met	Asn	Lys	Ile	Asp	Ala	Ile	Lys	Ala
		35					40					45			
Asp	Val	Ile	Ala	Gln	Ile	Thr	Ala	Glu	Val	Ala	Glu	Gly	Glu	Asp	Ile
	50					55					60				
Ser	Glu	Gly	Lys	Ile	Val	Asp	Ile	Phe	Thr	Ala	Leu	Glu	Ser	Gln	Ile
	65				70					75					80
Val	Arg	Ser	Arg	Ile	Ile	Ala	Gly	Glu	Pro	Arg	Ile	Asp	Gly	Arg	Thr
				85					90					95	
Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile	Cys	Thr	Gly	Val	Leu	Pro	Arg
			100					105					110		
Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	Gly	Glu	Thr	Gln	Ala	Leu	Ala
		115					120					125			
Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile	Ile	Asp	Glu	Leu
	130					135					140				
Thr	Gly	Glu	Arg	Ser	Asp	His	Phe	Leu	Phe	His	Tyr	Asn	Phe	Pro	Pro
145					150					155					160
Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro	Lys	Arg	Arg	Glu
			165						170					175	
Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg	Gly	Val	Ala	Ala	Val	Met	Pro
		180						185					190		
Thr	Leu	Ala	Glu	Phe	Pro	Tyr	Val	Val	Arg	Val	Val	Ser	Glu	Ile	Thr
		195					200					205			
Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys	Gly	Ala	Ser	Leu
	210					215					220				
Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile	Lys	Ala	Ala	Val	Ala	Gly	Ile
225					230					235					240
Ala	Met	Gly	Leu	Val	Lys	Glu	Asp	Glu	Lys	Phe	Val	Val	Leu	Ser	Asp
			245						250					255	
Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	Asp	Met	Asp	Phe	Lys	Val	Ala
		260						265					270		
Gly	Thr	Arg	Thr	Gly	Val	Thr	Ala	Leu	Gln	Met	Asp	Ile	Lys	Ile	Glu
		275					280					285			
Gly	Ile	Thr	Ala	Glu	Ile	Met	Gln	Ile	Ala	Leu	Asn	Gln	Ala	Lys	Ser
	290					295					300				

Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
305 310 315 320

Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
340 345 350

Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp
355 360 365

Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
370 375 380

Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
385 390 395 400

Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
405 410 415

Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
420 425 430

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
450 455 460

Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465 470 475 480

Asp Val Ala Ala Glu Glu Asn Ala
485

<210> 45
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<212> DNA
<213> Pasteurella multocida

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<222> (2)..(631)

<220>
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Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
20 25 30

gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145
Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
35 40 45

cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193

Arg	Val	Leu	Asn	Lys	Pro	Tyr	Arg	Gln	Gly	Phe	Val	Lys	Asn	Arg	Tyr		
50						55					60						
gta	gga	cgt	acg	ttt	att	atg	ccg	ggg	cag	gca	ttg	cga	gtc	agt	tct	241	
Val	Gly	Arg	Thr	Phe	Ile	Met	Pro	Gly	Gln	Ala	Leu	Arg	Val	Ser	Ser	80	
65					70				75								
gtt	aga	cgt	aaa	ctc	aat	acc	att	gct	tca	gaa	ttt	aaa	gat	aag	aat	289	
Val	Arg	Arg	Lys	Leu	Asn	Thr	Ile	Ala	Ser	Glu	Phe	Lys	Asp	Lys	Asn	95	
				85				90									
gtg	tta	tta	gtt	gac	gac	tcg	att	gta	cgt	ggg	acc	acg	tct	gaa	caa	337	
Val	Leu	Leu	Val	Asp	Asp	Ser	Ile	Val	Arg	Gly	Thr	Thr	Ser	Glu	Gln	110	
			100					105									
att	gtc	gaa	atg	gcg	aga	gcg	gca	ggg	gcg	aag	aaa	att	tat	ttt	gcc	385	
Ile	Val	Glu	Met	Ala	Arg	Ala	Ala	Gly	Ala	Lys	Lys	Ile	Tyr	Phe	Ala	125	
		115					120										
tct	gct	gca	cca	gaa	att	cgt	tat	cca	aat	gtg	tat	ggg	att	gat	atg	433	
Ser	Ala	Ala	Pro	Glu	Ile	Arg	Tyr	Pro	Asn	Val	Tyr	Gly	Ile	Asp	Met	140	
	130					135											
cca	acc	aaa	aat	gaa	ttg	atc	gct	tat	ggg	cgt	gat	gta	gat	gaa	att	481	
Pro	Thr	Lys	Asn	Glu	Leu	Ile	Ala	Tyr	Gly	Arg	Asp	Val	Asp	Glu	Ile	160	
					150					155							
gct	aac	tta	att	ggg	gtg	gat	aaa	ttg	att	ttc	caa	gat	ttg	gat	gcg	529	
Ala	Asn	Leu	Ile	Gly	Val	Asp	Lys	Leu	Ile	Phe	Gln	Asp	Leu	Asp	Ala	175	
				165				170									
tta	act	ggg	tct	gtg	caa	caa	gaa	aat	cca	agt	att	caa	gac	ttt	gat	577	
Leu	Thr	Gly	Ser	Val	Gln	Gln	Glu	Asn	Pro	Ser	Ile	Gln	Asp	Phe	Asp	190	
			180					185									
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Cys	Ser	Val	Phe	Thr	Gly	Val	Tyr	Val	Thr	Gly	Asp	Ile	Thr	Pro	Glu	205	
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Tyr	Leu																
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<211> 210

<212> PRT

<213> Pasteurella multocida

<400> 46

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			20					25					30				
Val	Ile	Pro	Val	Pro	Glu	Thr	Ser	Asn	Asp	Ile	Ala	Leu	Arg	Ile	Ala		
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Arg	Val	Leu	Asn	Lys	Pro	Tyr	Arg	Gln	Gly	Phe	Val	Lys	Asn	Arg	Tyr		
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Val	Gly	Arg	Thr	Phe	Ile	Met	Pro	Gly	Gln	Ala	Leu	Arg	Val	Ser	Ser		

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Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn						
		85		90		95
Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln						
		100		105		110
Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala						
		115		120		125
Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met						
		130		135		140
Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile						
		145		150		155
Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala						
		165		170		175
Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp						
		180		185		190
Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu						
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Tyr Leu						
		210				

<210> 47
 <211> 4788
 <212> DNA
 <213> Pasteurella multocida

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<220>
 <223> rci

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1				5				10										15	
att att ttt aga gat gta ata gaa cgc tat caa aat gaa gtg tct ata																			96
Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile																			
			20				25											30	
act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta																			144
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu																			
			35				40											45	
aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat																			192
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp																			

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gtt aga cgt gag ctt gtt act ata tcg tca gtg ctg aca aca gca ata Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile 85 90 95			288
aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys 100 105 110			336
cca aaa aac tcg gca gaa aga aaa gaa cga tat tca gaa cag gac att Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile 115 120 125			384
aaa aca ata tta gaa aca gct aga tat tgt gaa gat aaa cta ccc ata Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile 130 135 140			432
aca ctc aaa caa aga gta gca att gca atg tta ttt gct att gaa acc Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr 145 150 155 160			480
gct atg cgt gct ggt gag att gct agt ata aaa tgg gat aat gtt ttt Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe 165 170 175			528
ctt gaa aag aga ata gta cat tta ccg aca act aaa aac ggg cac tct Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser 180 185 190			576
aga gat gtg ccg ctt tcg caa aga gct gtt gcg cta att tta aaa atg Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met 195 200 205			624
aaa gag gta gaa aat gga gat ctt gtg ttt cag acc acg cct gaa tca Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser 210 215 220			672
tta agc acc acg ttt aga gtg tta aag aaa gag tgt gga ctt gaa cat Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His 225 230 235 240			720
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aga att tta caa aac aca tat tac gca ccg aat atg agt gaa gtg gca Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala 275 280 285			864
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gctcatcaat ccattctcga atttcagatt ggaaattttc taacgaatta ttttcattaa 2056
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 aactaaaacg tctggtgccc gaatttcacg atctaattt ttctgttgca attcagtcatt 4696
 atcaccaaga ttgggaacgt tagggtaatg gtaagctaatt actgcgcttg ggaattgctc 4756

4788

<213> Pasteurella multocida

Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
275 280 285

10a
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Asn Leu Leu Asp
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<210> 49

<211> 1618

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (2)..(1195)

<220>

<223> sopE

<400> 49

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Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile
1 5 10 15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt	97
Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly	
20 25 30	
att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat	145
Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn	
35 40 45	
gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga	193
Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly	
50 55 60	
aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc	241
Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val	
65 70 75 80	
aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac	289
Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp	
85 90 95	
gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc	337
Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile	
100 105 110	
aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa	385
Thr Glu Glu Gly Gln Tyr Thr Gln Leu Lys Ala Leu Leu Ile Ala Lys	
115 120 125	
aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac	433
Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp	
130 135 140	
aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac	481
Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn	
145 150 155 160	
gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg	529
Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala	
165 170 175	
gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg	577
Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met	

180										185										190										
ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac	Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp	625																												
195										200										205										
tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa	Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu	673																												
210										215										220										
cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc	Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser	721																												
225										230										235										
ggg gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat	Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp	769																												
245										250										255										
gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat	Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn	817																												
260										265										270										
ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc	Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe	865																												
275										280										285										
aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att	Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile	913																												
290										295										300										
gca ggg gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta	Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu	961																												
305										310										315										
gtg aaa gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc	Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr	1009																												
325										330										335										
aca aaa ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt	Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu	1057																												
340										345										350										
aac agt gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat	Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp	1105																												
355										360										365										
tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att	Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile	1153																												
370										375										380										
tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg	Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser	1195																												
385										390										395										
taaggggtag aaaatggctt taccacgcaa acttaaattg atgaatttaa tcatcgacgg 1255																														
taacaaatat ctcggcgaag tcacggaagt gactcaacca aaattagcaa tgaaaatcga 1315																														
agaatttcgc gcgggcggtg tgattgggtc ggtggatgtc aatctcgggc ttgaaaagct 1375																														
cgaagcggaa tttaaagccg gtggctacat ggtcgaatta attaaaaaat tcggcggggtc 1435																														
aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495																														

cacatctgtt gagcttgtga tgcaaggctg atttactgaa attgacagcg gaaacagcaa 1555
 agtgggcat gagactgaac aaacattcaa agtgccttta acgtattaca aaatcattgt 1615
 tga 1618

<210> 50
 <211> 398
 <212> PRT
 <213> Pasteurella multocida

<400> 50
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 1 5 10 15
 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
 20 25 30
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn
 35 40 45
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly
 50 55 60
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val
 65 70 75 80
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
 85 90 95
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
 100 105 110
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
 115 120 125
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
 130 135 140
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
 145 150 155 160
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
 165 170 175
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met
 180 185 190
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp
 195 200 205
 Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu
 210 215 220
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser
 225 230 235 240
 Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
 245 250 255
 Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
 260 265 270

Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
 275 280 285
 Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
 290 295 300
 Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
 305 310 315 320
 Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
 325 330 335
 Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
 340 345 350
 Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
 355 360 365
 Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
 370 375 380
 Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

<210> 51
 <211> 353
 <212> DNA
 <213> Pasteurella multocida

<220>
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 <222> (1)..(351)

<220>
 <223> unknown C1

<400> 51
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 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1 5 10 15
 cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30
 tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144
 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45
 gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60
 gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80
 aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95

gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110

gtc atc tat aaa aga ta 353
 Val Ile Tyr Lys Arg
 115

<210> 52
 <211> 117
 <212> PRT
 <213> Pasteurella multocida

<400> 52
 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1 5 10 15
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30
 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110
 Val Ile Tyr Lys Arg
 115

<210> 53
 <211> 509
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1) .. (507)

<220>
 <223> unknown C2

<400> 53
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 Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1 5 10 15
 gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96
 Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
 20 25 30
 cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt 144
 Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser

35					40					45						
gaa	gag	aat	tgc	ttt	gaa	tat	tac	aat	gag	cgt	aat	gag	ccc	acg	ttt	192
Glu	Glu	Asn	Cys	Phe	Glu	Tyr	Tyr	Asn	Glu	Arg	Asn	Glu	Pro	Thr	Phe	
50					55					60						
tct	tcc	ttt	gga	ttt	gaa	ggg	ttt	gag	aca	gag	cgg	tct	agc	gcc	tct	240
Ser	Ser	Phe	Gly	Phe	Glu	Gly	Phe	Glu	Thr	Glu	Arg	Ser	Ser	Ala	Ser	
65					70					75					80	
ctt	gaa	aat	ata	tat	gct	cag	tat	att	tat	gat	gat	cca	atc	tat	ggg	288
Leu	Glu	Asn	Ile	Tyr	Ala	Gln	Tyr	Ile	Tyr	Asp	Asp	Pro	Ile	Tyr	Gly	
85					90					95						
tat	gaa	cat	gtg	tat	tct	ttt	ggg	agt	act	ggc	gag	gga	cat	ttt	atc	336
Tyr	Glu	His	Val	Tyr	Ser	Phe	Gly	Ser	Thr	Gly	Glu	Gly	His	Phe	Ile	
100					105					110						
tgt	ttt	gat	tat	cgt	gat	gat	cca	aaa	ggg	gat	gaa	ccc	aaa	atc	tgt	384
Cys	Phe	Asp	Tyr	Arg	Asp	Asp	Pro	Lys	Gly	Asp	Glu	Pro	Lys	Ile	Cys	
115					120					125						
atc	gtg	att	cac	gat	gaa	tat	gat	gaa	aaa	aca	ggg	aaa	atg	cga	ctg	432
Ile	Val	Ile	His	Asp	Glu	Tyr	Asp	Glu	Lys	Thr	Gly	Lys	Met	Arg	Leu	
130					135					140						
ttt	cct	ata	gca	gag	aat	ttt	gaa	gcg	ttt	tta	gat	agt	ttg	aaa	tca	480
Phe	Pro	Ile	Ala	Glu	Asn	Phe	Glu	Ala	Phe	Leu	Asp	Ser	Leu	Lys	Ser	
145					150					155					160	
ttt	gat	gaa	atg	ata	gag	aag	tat	tcg	ta						509	
Phe	Asp	Glu	Met	Ile	Glu	Lys	Tyr	Ser								
165																

<210> 54

<211> 169

<212> PRT

<213> Pasteurella multocida

<400> 54

Met	Lys	Asn	Phe	Arg	Asn	Ile	Asn	Ile	Tyr	Ser	Asp	Tyr	Gly	Lys	Val
1				5					10					15	
Asp	Lys	Glu	Ile	Ile	Leu	Glu	Phe	Glu	Asn	Glu	Phe	Asn	Ile	Lys	Leu
			20					25					30		
Pro	Ser	Leu	Tyr	Ile	Asp	Leu	Ile	Thr	Ala	His	Asn	Ala	Pro	Lys	Ser
		35					40					45			
Glu	Glu	Asn	Cys	Phe	Glu	Tyr	Tyr	Asn	Glu	Arg	Asn	Glu	Pro	Thr	Phe
		50				55					60				
Ser	Ser	Phe	Gly	Phe	Glu	Gly	Phe	Glu	Thr	Glu	Arg	Ser	Ser	Ala	Ser
		65				70				75					80
Leu	Glu	Asn	Ile	Tyr	Ala	Gln	Tyr	Ile	Tyr	Asp	Asp	Pro	Ile	Tyr	Gly
			85					90						95	
Tyr	Glu	His	Val	Tyr	Ser	Phe	Gly	Ser	Thr	Gly	Glu	Gly	His	Phe	Ile
			100					105					110		

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
 115 120 125
 Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
 130 135 140
 Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
 145 150 155 160
 Phe Asp Glu Met Ile Glu Lys Tyr Ser
 165

<210> 55
 <211> 443
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(441)

<220>
 <223> unknown C3

<400> 55
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 1 5 10 15
 ggt aaa aac gaa agt aat aaa gat att tta aaa tta gta gaa ata gtt 96
 Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
 20 25 30
 tct tca gat ttt gaa gtg gat gaa cta agt cat aaa gat gaa cac gag 144
 Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
 35 40 45
 ata tat tat ttg ttt tat aag agg ggt gtt gaa ttt tgt ttt aaa aga 192
 Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
 50 55 60
 ata gat gaa gag tat gtc tta tat tcg gtt ttc ttt ttc ttg gta gag 240
 Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
 65 70 75 80
 gtt gat aat tat ttt tca tgc cca ttt att cat gaa tta ata tgt gat 288
 Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
 85 90 95
 ctt aaa cac gga ttc tca ata gag gat att ata agg ttt tta ggg gag 336
 Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
 100 105 110
 cca aat ttt aaa ggt agt ggc tgg gta aga tat tct tat aat gga aga 384
 Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
 115 120 125
 aat att cat ttc gaa ttt aat gaa tct aat gaa tta tcc cag att agc 432
 Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
 130 135 140
 att ttt att ta 443

Ile Phe Ile
145

<210> 56
<211> 147
<212> PRT
<213> Pasteurella multocida

<400> 56
Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
1 5 10 15
Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
20 25 30
Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
35 40 45
Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
50 55 60
Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
65 70 75 80
Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
85 90 95
Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
100 105 110
Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
115 120 125
Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
130 135 140
Ile Phe Ile
145

<210> 57
<211> 8498
<212> DNA
<213> Pasteurella multocida

<220>
<223> unknown C

<400> 57
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caattatcaa ttgttgaaat ttatcctttc aatgaagaac aagggatacg ttttcataat 120
aaaagtgtgg tacaacttaa accagaagag gtggaatggc catcaatcca ttatcttttc 180
tttgctggcg atattcagca agtcgctcat ctgcgaaag ccgcagaaat gggttgcgtg 240
gtgattgata tgaaagggat ttgtgccagc ttgcaagacg tccctgtggg gataccggga 300
gtaaatacagg aaaaattggg agatttacgt cagcgtaata ttgtgtcctt agccgatcca 360
caagtgcac aacttgcatt agtcatcgcc tcgttgatgt caaatcacga aatcaaagac 420

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acg	att	gac	caa	att	tcc	cag	ttt	gat	ggc	tca	aac	aga	cgt	tat	gat	3897	
Thr	Ile	Asp	Gln	Ile	Ser	Gln	Phe	Asp	Gly	Ser	Asn	Arg	Arg	Tyr	Asp		
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Glu	Leu	Asn	Ile	Val	Arg	Pro	Ser	Gly	Trp	Thr	Ser	Ala	Ser	Ser	Gly		
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 Thr Cys Gln Ile Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu
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 450 455 460
 Lys Asn Pro Asp Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg
 465 470 475 480
 Val Ile Leu Val Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser
 485 490 495
 Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu
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 Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg
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 Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys
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aag aaa atc gtt ttt gtt agt tta gct tta tct gtc gtt ggt tgt tct 763
Lys Lys Ile Val Phe Val Ser Leu Ala Leu Ser Val Val Gly Cys Ser
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acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca 811
Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr
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Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser Thr Gln Asn Tyr Ser Ala
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ctc att tca ctg tat cgc gat gtg ttg aaa gcc aaa gaa gat cct tca 907
Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys Ala Lys Glu Asp Pro Ser
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Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr Gln Arg Gly Asp Ser Lys
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tct tct tta ctt tat tta acg cca tta ctg aat gat aat acg aag ctt 1003
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Asn Gly Asn Leu Val Asn Ala Arg Asn Asp Ile Asn Lys Ala Arg Glu	
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Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp Leu Ile Asn Ala Leu Lys	
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 Ile His Asn Leu Val Phe Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr
 210 215 220
 Ala Lys Asp Ile Ile Val Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp
 225 230 235 240
 Leu Ile Asn Ala Leu Lys Lys Thr Thr His Val Ser Lys Gly Val Thr
 245 250 255

Arg

<210> 62

<211> 1788

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(600)

<220>

<223> unknown K

<400> 62

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Val	Asn	Thr	Gly	Leu	Ile	His	Ser	Asn	Gly	Asn	Ala	Lys	Leu	Thr	Phe	
1				5					10					15		
aaa	gat	gac	acc	agt	ttt	gtg	act	gaa	gga	aat	aac	ttt	atc	aca	gca	96
Lys	Asp	Asp	Thr	Ser	Phe	Val	Thr	Glu	Gly	Asn	Asn	Phe	Ile	Thr	Ala	
			20						25					30		

aaa gac aac tta gaa atc acg gca aaa aat gtt caa att gat caa gcg	144
Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala	
35 40 45	
aaa aat att caa tta aac gcg aat atc acg atc aat acc aag tct ggt	192
Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly	
50 55 60	
ttt gtg aat tac ggt acc tta gca agt gct caa aat tta acg att aat	240
Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn	
65 70 75 80	
acc gaa caa ggc agc att tat aac ata ggc ggt atc ttg ggg gcg ggt	288
Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly	
85 90 95	
aaa agt ttg aat ctg agc gcg aaa aga gga gaa aac caa gga gga tat	336
Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr	
100 105 110	
ctt att aat caa ggt aag agt cta ctc cat tct gaa ggc gcc atg aac	384
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn	
115 120 125	
ctc aca gcg gat cgc acg gtg tac aat tta ggg aat att ttt gct aaa	432
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys	
130 135 140	
ggg gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc	480
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu	
145 150 155 160	
aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat	528
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr	
165 170 175	
tat cgt atc aat gaa acg gca aaa cat ggt tgg cat aat aac ttc tat	576
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr	
180 185 190	
gaa tta aac gtc gac aga gtt tct tgatttggtgc atcaattttg taaccaccgg	630
Glu Leu Asn Val Asp Arg Val Ser	
195 200	
ttaataaaac accagcaatt tcaacgccat tcatggcaga taatgccgct gcgacgatca	690
catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat	750
tggtcaaatt acgtgcacag aaagtgatgc cacgaatgcg acgttcattg atcgcgcctt	810
catgaataat ggcagcacct aaatgttttg ctaaataaat ggcacgagtc gcaattaatt	870
ctgcgctcca aggaatacat gccagattt taattgggct tttctcaaataaatgataaa	930
tctcagatac ttgattttgt gtgtgttggga aagaatcaaaa aatttctgcc aagtcagggc	990
gagtacgacc agattcatca atcggcgcgcat taaatttatt gatcacaaca ccaagtaaata	1050
tagggttatt tttgctgcc aataatgagg ctgcggcttt gatgcgttct ttgagttctg	1110
ccggtgtttc cgtcgccggg gctgcaacaa gaatgatttc cgcatacaagt gcttgagcaa	1170
tttcatagtt aatgctattg gcataagaat gcttacgcgt agggattaaa ccttccacca	1230

cgacaatttc attgtttttg gcgagttgtt gatgattttc aacaattttt tctagtagca 1290
catcagattg attttgaccg atgagtgatt cagctacact taacataaat ggttcactgg 1350
tttcaatggg ggtactgggt cgaataattg atgttggtgc atcaatcata tcttcacctg 1410
agttcggctg agaaattggg ttcataaagc cgactttcgc ccctttttgc tccagtgcac 1470
gtgttaaacc taagctgaca ctgggtaagc ctacaccagc actaatcggg ataaggataa 1530
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gaatcggcag ttaattgatc tttacgcgat gcaaaggcgc gcggtatctt gtgcaataac 1650
aagttcttca ttcgttgga tcaccatggc aacaggcgta ttgtctgctg taatcacccc 1710
ttcatgacca aagcgagccg ctttgttttt atctgaatcc acttgataac cgaacagttt 1770
taaagtgttt aaggttga 1788

<210> 63
<211> 200
<212> PRT
<213> Pasteurella multocida

<400> 63
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1 5 10 15
Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
20 25 30
Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
35 40 45
Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
50 55 60
Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
65 70 75 80
Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
85 90 95
Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
100 105 110
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
115 120 125
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys
130 135 140
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
145 150 155 160
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
165 170 175
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
180 185 190

Glu Leu Asn Val Asp Arg Val Ser
 195 200

<210> 64
 <211> 278
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (108)..(278)

<220>
 <223> unknown O

<400> 64
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 cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116
 Met Lys Ile
 1
 act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164
 Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
 5 10 15
 gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212
 Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu
 20 25 30 35
 gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260
 Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu
 40 45 50
 agc aaa agg gga cat agt 278
 Ser Lys Arg Gly His Ser
 55

<210> 65
 <211> 57
 <212> PRT
 <213> Pasteurella multocida

<400> 65
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1 5 10 15
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
 20 25 30
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
 35 40 45
 Glu Glu Glu Ser Lys Arg Gly His Ser
 50 55

<210> 66
 <211> 1020
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(597)

<220>
 <223> unknown P

<400> 66

gtc aac aca tca aaa gtt gag att gac tat gcc gtc act cgt gcg gcg	48
Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala	
1 5 10 15	
gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att	96
Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile	
20 25 30	
tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat	144
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr	
35 40 45	
ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa	192
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln	
50 55 60	
ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta	240
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu	
65 70 75 80	
cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc	288
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg	
85 90 95	
act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca	336
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala	
100 105 110	
gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca	384
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala	
115 120 125	
atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc	432
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly	
130 135 140	
ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa	480
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys	
145 150 155 160	
gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc	528
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu	
165 170 175	
gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat	576
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp	
180 185 190	
ttt tca aat cgt tta gca tcg taaggggtag aaaatggctt taccacgcaa	627
Phe Ser Asn Arg Leu Ala Ser	
195	
acttaaattg atgaatttaa tcatcgacgg taacaaatat ctcggcgaag tcacggaagt	687
gactcaacca aaattagcaa tgaaaatcga agaatttcgc gcgggcggta tgattgggtc	747

ggtggatgtc aatctcgggc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat 807
 ggtcgaatta attaaaaaat tcggcggggtc aatcaacggc attccattgc gttttcttgg 867
 ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttgtga tgcaagggtcg 927
 atttactgaa attgacagcg gaaacagcaa agtgggcgat gacactgaac aaacattcaa 987
 agtgccttta acgtattaca aaatcattgt tga 1020

<210> 67
 <211> 199
 <212> PRT
 <213> Pasteurella multocida

<400> 67
 Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
 1 5 10 15
 Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
 20 25 30
 Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
 35 40 45
 Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
 50 55 60
 Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
 65 70 75 80
 Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
 85 90 95
 Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
 100 105 110
 Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
 115 120 125
 Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
 130 135 140
 Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
 145 150 155 160
 Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
 165 170 175
 Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
 180 185 190
 Phe Ser Asn Arg Leu Ala Ser
 195

<210> 68
 <211> 2584
 <212> DNA
 <213> Pasteurella multocida

<220>

<222> (1042) .. (2286)

<220>

<223> xylA

<400> 68

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taccattatt ttatggaatc tctctggacc gatgaccatt gccaatattg aaattcctca 120
cgcgatgggc tttttggtct ttatttacgt gctgttttagc agtattgtgg catttaaaat 180
cggtcgcccg ttaattcagc tcaattttgc caatgaacgc ttaaacgcca actaccgtta 240
ttcacttata cgtctgaaag aatatgctga aagcattgct ttttatcgtg gtgaaaaaat 300
ggaaaaacgt ctattgacca cacaatttaa tcaggtgatt gataacgttt ggcaagtaat 360
ctaccgcacc ttgaaattat ccggttttaa cttaatcatt acgcagattt cgggtggtttt 420
tccgctgggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgaggggtgtt 480
agaatagcga tactttctgt tggaaaagta aactctttaa tataaataga aatcgcttga 540
atgattctcg ggcaaaaaat aatgtactca tttgcgatct catactgata atggcggaagt 600
aaatatcttc ttacaatatt atggtaatta tcaggtaata ccgtatagcc atagattcca 660
gttctatttt gttttgctaa ataattgatg agcatttgag gcgcaggtaa atccatatct 720
gcaacagaca ttgaaatcat atccttgccg tatttacgag taattgccca tttagcacta 780
tgacaatctg atctatcagt aaaaacatca aacaaattat ccgtcataca tgttctccaa 840
tattggattt atataaactt tagaacttga ggtagattgt tggaattgtt aaatctggta 900
tttctattac gttttttctt ttttgtgata taagccacaa taaccaataa tcttaattgt 960
taagtgaat aacgtaattg atcctcccat tgttttacta aattatgtct ctgaaactta 1020
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tttgttcagg agaaatcatt t atg tcc act tac ttc gac aaa att gaa aaa 1071
Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys
1 5 10

gta aat tat gaa ggt gta act tca tct aat ccg ttt gca tat aag cat 1119
Val Asn Tyr Glu Gly Val Thr Ser Ser Asn Pro Phe Ala Tyr Lys His
15 20 25

tat gat gct aat caa gtt att tta ggt aag acg atg gct gaa cac tta 1167
Tyr Asp Ala Asn Gln Val Ile Leu Gly Lys Thr Met Ala Glu His Leu
30 35 40

cgt tta gcc gtc tgt tat tgg cac act ttc tgt tgg aca ggg aat gat 1215
Arg Leu Ala Val Cys Tyr Trp His Thr Phe Cys Trp Thr Gly Asn Asp
45 50 55

atg ttc ggt gtc ggt tct ttc gat cgt tgt tgg cag aag gcg agt gat 1263
Met Phe Gly Val Gly Ser Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp
60 65 70

tca tta gca ggt gca aaa caa aaa gca gat atc gct ttt gaa ttt ttc 1311
Ser Leu Ala Gly Ala Lys Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe

75	80	85	90	
agt aaa tta ggc ata cct tat tat tgt ttt cat gat gtt gat gtt gcg Ser Lys Leu Gly Ile Pro Tyr Tyr Cys Phe His Asp Val Asp Val Ala 95 100 105				1359
cca gaa ggt cat tca ttt aaa gaa tat ttg tgc aac ttt aat aca atg Pro Glu Gly His Ser Phe Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met 110 115 120				1407
atc gat gtt tta gcg cag aaa caa gaa gaa aca ggc gtc aaa ttg ttg Ile Asp Val Leu Ala Gln Lys Gln Glu Glu Thr Gly Val Lys Leu Leu 125 130 135				1455
tgg ggg act gca aat tgt ttt aca cac cct cgt tat atg tct ggt gct Trp Gly Thr Ala Asn Cys Phe Thr His Pro Arg Tyr Met Ser Gly Ala 140 145 150				1503
gca aca aat ccg aat cca gaa att ttt gct tgg gct gct gca caa gta Ala Thr Asn Pro Asn Pro Glu Ile Phe Ala Trp Ala Ala Gln Val 155 160 165 170				1551
ttt act gcc atg ggg gca act cag cgt tta ggt ggt gaa aat tat gtt Phe Thr Ala Met Gly Ala Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val 175 180 185				1599
ttg tgg gga gga cgt gaa gga tat gaa acg tta tta aat acc aat tta Leu Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu 190 195 200				1647
aaa cag gag cga gag caa att gga cgt ttc atg caa atg gtg gtt gag Lys Gln Glu Arg Glu Gln Ile Gly Arg Phe Met Gln Met Val Val Glu 205 210 215				1695
cat aaa tat aaa atc ggt ttt aac ggg act ttg ctg att gaa cca aag His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Ile Glu Pro Lys 220 225 230				1743
cca caa gag cca acg aaa cat caa tat gac tat gat gtg gcg acc gtt Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val 235 240 245 250				1791
tat ggc ttt tta aag cag ttt ggt tta gaa aaa gaa att aaa gtg aat Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn 255 260 265				1839
att gaa gct aat cac gca aca tta gct gga cac act ttc cag cat gaa Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu 270 275 280				1887
gtc gcc atg gct aca gcg tta gat att ttt ggt tct att gat gca aat Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn 285 290 295				1935
cgt ggt gat cca caa tta ggt tgg gat acc gat caa ttc cct aat agc Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser 300 305 310				1983
gta gaa gaa aat act ttg gtc ata tat gaa att ctc aaa gca ggg ggc Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly 315 320 325 330				2031
ttt aca acc ggt ggt ttt aat ttt gat gct aaa atc cgt cgg cag agt				2079

Phe Thr Thr Gly Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser
 335 340 345
 acg gat cct tac gat tta ttt cat gga cat att ggc gcg att gat gta 2127
 Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val
 350 355 360
 ctt gcc tta tca cta aaa tgt gcg gcg aaa atg ctt gaa gag caa gct 2175
 Leu Ala Leu Ser Leu Lys Cys Ala Ala Lys Met Leu Glu Glu Gln Ala
 365 370 375
 tta caa aaa gtc gtc aat caa cgt tat gct ggt tgg aca tca tca ctt 2223
 Leu Gln Lys Val Val Asn Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu
 380 385 390
 ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga 2271
 Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg
 395 400 405 410
 cta aca aaa gtg ctt taaaacgttc eggcttacgc cagacatcta gacgattgaa 2326
 Leu Thr Lys Val Leu
 415
 taatttcaat attgtctccg cacgtaattc aaaggctttg tgtatgtgcg aatgatattc 2386
 acaacaaagt tctgcaaaat cttgaattgc gtgaggtaat ttaaagcgct gacataagcg 2446
 tcttgctggc atgacaccag ctttttcatg tccataatga tgtggcaata tttcttttgg 2506
 tgtaaggct tttcctaaat catgacaaat tgcagcaaaa cgtaccgcac ttttgtcact 2566
 gtccgtgttt tctgtcga 2584

 <210> 69
 <211> 415
 <212> PRT
 <213> Pasteurella multocida

 <400> 69
 Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys Val Asn Tyr Glu Gly Val
 1 5 10 15
 Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val
 20 25 30
 Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr
 35 40 45
 Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
 50 55 60
 Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys
 65 70 75 80
 Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro
 85 90 95
 Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
 100 105 110
 Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
 115 120 125

Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
 130 135 140
 Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
 145 150 155 160
 Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
 165 170 175
 Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
 180 185 190
 Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
 195 200 205
 Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
 210 215 220
 Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
 225 230 235 240
 His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
 245 250 255
 Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
 260 265 270
 Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala
 275 280 285
 Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu
 290 295 300
 Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu
 305 310 315 320
 Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe
 325 330 335
 Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu
 340 345 350
 Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys
 355 360 365
 Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn
 370 375 380
 Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile
 385 390 395 400
 Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu
 405 410 415

<210> 70

<211> 3501

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (298)..(1905)

<220>

<223> yabk

<400> 70

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aatgcctgtg cggatcattt ccttgccctt ttacttcata cagaagcaca agggcattta 120
gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180
cttagagcca cccaaatgaa cacgaaagtg ctcgatacct caaaagtgaa tgccgaacaa 240
gtcaaaaaat ggattgctgt ttggcaaacg accctaaccc aataattgtt tgtcttg 297

atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt 345
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
  1             5             10             15

ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc 393
Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
             20             25             30

tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg 441
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
             35             40             45

ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa 489
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln
             50             55             60

gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt gcc att gta gca 537
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala
             65             70             75             80

cga gcc ttt ttt tat caa ccg ttt gtg ggc aag aaa ctg atc ctc aaa 585
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys
             85             90             95

tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggt 633
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly
             100             105             110

tta tta ggc gtg tat ggc gct tct ggc tgg tta gcg atg tta agc cag 681
Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
             115             120             125

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Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile
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Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe
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Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala
             165             170             175

caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc 873
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro
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Tyr	Leu	Arg	Gln	Gln	Leu	Leu	Pro	Ala	Phe	Thr	Leu	Ile	Phe	Met	Leu	
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Cys	Phe	Thr	Ser	Phe	Ala	Ile	Val	Leu	Thr	Leu	Gly	Gly	Gly	Pro	Lys	
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gat	gta	ccg	aaa	gcc	ggc	tta	ttt	gcg	tta	tta	caa	ttt	gtt	ttt	tgt	1065
Asp	Val	Pro	Lys	Ala	Gly	Leu	Phe	Ala	Leu	Leu	Gln	Phe	Val	Phe	Cys	
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Phe	Leu	Leu	Phe	Thr	Leu	Ser	Ser	Phe	Phe	Ser	Pro	Ala	Pro	Ala	Thr	
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Thr	Leu	His	Ser	Gln	Pro	Thr	Trp	Phe	Ala	Pro	Gln	Ser	Tyr	Trp	Val	
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Lys	Leu	Trp	Gln	Arg	Met	Ile	Ile	Val	Cys	Ala	Thr	Val	Phe	Ile	Leu	
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gcc	tta	tta	ttg	ctt	gcc	aga	gaa	tta	cat	tgg	cga	cat	tat	cgc	agc	1401
Ala	Leu	Leu	Leu	Leu	Ala	Arg	Glu	Leu	His	Trp	Arg	His	Tyr	Arg	Ser	
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Asn	Met	Ile	Tyr	Tyr	Glu	Lys	Leu	Cys	Gln	Ser	Leu	Asn	Leu	Arg	Gly	

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Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met			
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Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr			
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gca atc gcg tta ttt ggt cag gct gac ttc aca tcg tta ccg cat ttg			1785
Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu			
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Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu			
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Arg His Gln Glu Pro Arg Asp Asp			
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Arg	Ala	Phe	Phe	Tyr	Gln	Pro	Phe	Val	Gly	Lys	Lys	Leu	Ile	Leu	Lys	85	90	95	
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Gln	Leu	Asn	Leu	Arg	Gly	Trp	His	Phe	Ile	Arg	Leu	Ile	Glu	Trp	Pro	180	185	190	
Tyr	Leu	Arg	Gln	Gln	Leu	Leu	Pro	Ala	Phe	Thr	Leu	Ile	Phe	Met	Leu	195	200	205	

Cys 210	Phe	Thr	Ser	Phe	Ala	Ile 215	Val	Leu	Thr	Leu	Gly 220	Gly	Gly	Pro	Lys
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Leu 305	Pro	Leu	Leu	Asn	Thr 310	Leu	Val	Ser	Ala	Leu 315	Leu	Ser	Ser	Gln	Phe 320
Phe	Thr	Leu	Trp	Leu 325	Gln	Pro	Gln	Leu	Trp 330	Lys	Ala	Leu	Gly	Tyr 335	Ser
Leu	Thr	Ile	Ala 340	Pro	Thr	Ser	Ala	Leu 345	Leu	Ala	Leu	Val	Leu 350	Ser	Phe
Ala	Leu	Leu 355	Leu	Leu	Ala	Arg	Glu 360	Leu	His	Trp	Arg	His 365	Tyr	Arg	Ser
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Thr 385	Leu	Val	Leu	Ala	Ile 390	Gly	Leu	Phe	Ile	Leu 395	Leu	Arg	Glu	Ile	Asp 400
Phe	Ser	Pro	Tyr	His 405	Leu	Phe	Gly	Val	Val 410	Val	Cys	Cys	Asn	Ala 415	Leu
Ala	Ala	Met	Pro 420	Phe	Val	Leu	Arg	Ile 425	Leu	Ala	Leu	Pro	Met 430	His	Asn
Asn	Met	Ile 435	Tyr	Tyr	Glu	Lys	Leu 440	Cys	Gln	Ser	Leu	Asn 445	Leu	Arg	Gly
Trp 450	Gln	Arg	Phe	Arg	Leu	Ile 455	Glu	Trp	His	Lys	Leu 460	Arg	Ala	Pro	Met
Lys 465	Tyr	Ala	Phe	Ala	Leu 470	Ala	Cys	Ala	Leu	Ser 475	Leu	Gly	Asp	Phe	Thr 480
Ala	Ile	Ala	Leu	Phe 485	Gly	Gln	Ala	Asp	Phe 490	Thr	Ser	Leu	Pro	His 495	Leu
Leu	Tyr	Gln	Gln 500	Leu	Gly	His	Tyr	Arg 505	Ser	Gln	Glu	Ala	Ala 510	Val	Thr
Ala	Phe	Ile 515	Leu	Leu	Val	Phe	Cys 520	Leu	Ser	Val	Phe	Met 525	Ile	Ile	Glu
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Ser	Phe	His	Ser	Thr	Asn	Val	His	Arg	Gly	Thr	Phe	Val	Gly	Arg	Gly	
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Thr	Phe															
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ttc	ctttttct	ttcgtaaacg	tttccactta	gattgcccag	aagccgatct	gtctgaatgg										2979
gaacaagtgt	tataccaaga	agcgaatcca	acaggtgaag	tggtgatcgg	tatgggtgggt											3039
aaatacactg	aattaccgga	tgccatacaa	tcggttaatg	aagccttgaa	acacgcaggc											3099

ttaaaaaacc gtcttagcgt gcaaatcaaa tatattgatt cacaagatgt ggaaaccaa 3159
 ggcacagaag tgttagaagg cgt 3182

<210> 73
 <211> 422
 <212> PRT
 <213> Pasteurella multocida

<400> 73
 Met Pro His His Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His
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 Leu Tyr Lys Ile Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile
 20 25 30
 Gly Ile Gly Thr Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe
 35 40 45
 Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile
 50 55 60
 Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser
 65 70 75 80
 Arg Val Thr Asp Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met
 85 90 95
 Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp
 100 105 110
 Leu Tyr Asn Ala Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile
 115 120 125
 Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly
 130 135 140
 Ile Ile Gly Gly Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln
 145 150 155 160
 Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val
 165 170 175
 Ala Gly Gly Ala Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile
 180 185 190
 Ile Tyr Gly Met Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala
 195 200 205
 Ala Ile Pro Ala Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile
 210 215 220
 Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser
 225 230 235 240
 Ser Glu Asn His Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His
 245 250 255
 Asp Ile Ala Ile Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile
 260 265 270

Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val
 275 280 285
 Gly Val Ile Leu Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile
 290 295 300
 Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile
 305 310 315 320
 Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met
 325 330 335
 Gly Gly Asp Arg Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser
 340 345 350
 Pro Ile Tyr Thr Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly
 355 360 365
 Met Phe Leu Asp Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr
 370 375 380
 Ser Lys Ala Thr Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile
 385 390 395 400
 Trp Arg Gly Pro Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe
 405 410 415
 Val Gly Arg Gly Thr Phe
 420

<210> 74
 <211> 2787
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (463) .. (936)

<220>
 <223> yhcJ

<400> 74
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 gcatacaaag caagaatggt ggccagtgtg tcatgcatcg cattggcagc atcagcttgt 120
 ggcgttgcaa tctgttggtg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
 tttgttccac caatatctaa tgctaaacag cgcataggct ctccttctgt gatgacttat 240
 tttgccgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgca 300
 gatcctacgg tgacagagta agcaccaatc tcaattgcgg ttttcgccaa ttctggggtg 360
 ttatagcgcc cttctgccat cactcggcag ccagcagcat tcaaattctt gactaactga 420
 taatccggtt cagctggaat ttcaccgcca gtataaccag ac atg gtg cta cca 474
 Met Val Leu Pro

1

ata att tct acc cct aag ttg tgg caa tac atc cct tct tca aaa tta 522

Ile	Ile	Ser	Thr	Pro	Lys	Leu	Trp	Gln	Tyr	Ile	Pro	Ser	Ser	Lys	Leu	
5					10				15					20		
gaa	caa	tcc	gcc	atg	gct	aaa	caa	cct	aat	tct	ttg	att	cgt	tta	ata	570
Glu	Gln	Ser	Ala	Met	Ala	Lys	Gln	Pro	Asn	Ser	Leu	Ile	Arg	Leu	Ile	
				25				30					35			
atg	gct	tca	cgt	gta	gtt	gga	cgg	acg	cga	tcg	gta	cca	tca	aaa	gca	618
Met	Ala	Ser	Arg	Val	Val	Gly	Arg	Thr	Arg	Ser	Val	Pro	Ser	Lys	Ala	
			40				45					50				
ata	ata	tcg	gcg	cct	gct	gcg	gct	aac	tct	tca	atg	tct	tgt	aaa	aat	666
Ile	Ile	Ser	Ala	Pro	Ala	Ala	Ala	Asn	Ser	Ser	Met		Ser	Cys	Lys	Asn
		55				60					65					
ggg	cta	ata	cga	acg	gga	ctg	tca	ggt	aaa	tcg	cgt	tta	acg	ata	cca	714
Gly	Leu	Ile	Arg	Thr	Gly	Leu	Ser	Gly	Lys	Ser	Arg	Leu	Thr	Ile	Pro	
	70				75					80						
ata	atc	ggt	aca	ttg	acg	acg	tta	cgc	gtg	gct	ttt	aaa	ttt	tcg	atc	762
Ile	Ile	Gly	Thr	Leu	Thr	Thr	Leu	Arg	Val	Ala	Phe	Lys	Phe	Ser	Ile	
	85			90				95							100	
cct	tca	ata	cgt	aac	ccg	gca	gca	cca	ccg	ata	acg	gat	gct	tgc	gcc	810
Pro	Ser	Ile	Arg	Asn	Pro	Ala	Ala	Pro	Pro	Ile	Thr	Asp	Ala	Cys	Ala	
				105				110						115		
atg	gcg	gca	aca	att	tct	ggc	gag	tcc	att	ggc	cca	tta	tct	acg	ggc	858
Met	Ala	Ala	Thr	Ile	Ser	Gly	Glu	Ser	Ile	Gly	Pro	Leu	Ser	Thr	Gly	
			120				125					130				
tgg	caa	gat	gcg	att	aag	cca	tat	tta	att	tgt	tct	aaa	act	tgc	gga	906
Trp	Gln	Asp	Ala	Ile	Lys	Pro	Tyr	Leu	Ile	Cys	Ser	Lys	Thr	Cys	Gly	
		135					140					145				
tgt	gat	agt	ttt	gac	ata	tta	act	cca	gtc	ttaa	tttatc	aaaaga	aat			956
Cys	Asp	Ser	Phe	Asp	Ile	Leu	Thr	Pro	Val							
	150					155										
tgactccaat	ttgcataggt	taatccttaga	attaaaaaat	aacaacccaaa	ataataaaaa											1016
tttgagatct	ttgtcgcata	tttattcata	gggaatagac	agcttaattt	tagttatgat											1076
ttgtcaatcc	ttgtattttt	ttgtgtttgc	tggtttgcga	tacactgttc	taatattgct											1136
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tgattgaccg	gtgtggcttc	taataaaaaag	tagtgggacg	taggagaaat	ggtgtgtagg											1376
tgagtcagaa	tgatctttaa	ctatcgcatg	acttgcgccg	gtgaatacgt	ttcttcctta											1436
caaatatcat	tgacgcctaa	aaaaagaaaa	acagattgtc	caagttgttg	aatccgttta											1496
ggtttaacga	taacatccaa	atattgtcgc	gtactgacgc	cagaaagtcc	taaattggcg											1556
acggtttgtc	ccgctaattg	agggtgtgcct	gctacctggt	cgtcccacat	gtcaaaaagt											1616
gaatgaccaa	ttaagctgat	attggcaggt	ttggaaaatt	ccgccatttt	gctctgatag											1676

cgttgataaa tatcctgatac acttagcatg tgtggacctc tattttgaaa taaaacgcta 1736
 agtattatat aaaacctgat atgccggtaa acagtaaact tatcttccgt aggggtaaatt 1796
 attcaatttt gtgacgaacc tatcatttat gaaataaaac ttcattttct atataaaaaa 1856
 tagttttttc actttagaat gccaaacgtg tgaaatttat ttcacatca ttttaacgta 1916
 atcccaacgt aaccaataga ggagaactca taatgaaatt taaaaaacta ctacttgcac 1976
 ctttatgttt aggtgtttca gcttctgtat ttgcagcaga ttacgatctt aaattcggtg 2036
 tgggtgctggg tccaagctca aacgaatata aagcagtaga attctttgctg aaagaagtga 2096
 aagaaaaatc caatggcaaa attgatgtgg ctattttccc tagctcacag ttaggtgatg 2156
 accgtgtgat gattaaacaa ttaaaagacg gtgcattaga ctttacgtta ggtgaatcag 2216
 cacgtttcca aatttacttc ccagaagcag aagtatttgc gttgccttat atgattccta 2276
 attttgaaac ctctaaaaaa gcgttgctcg acacaaaatt tgggtcaagggt ttattgaaaa 2336
 aaattgataa agagttaaac gtacaagtgt tatctgtggc gtataacgggt acacgtcaaa 2396
 caacttctaa ccgtgcaatc aacagcattg aagacatgaa aggggttaaaa ttacgtgtac 2456
 ctaacgcggc aaccaacctt gcttatgcaa aatacgtggg tgcagcgcca acaccaatgg 2516
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 acatcttaaa tgaccaactt tacttaatca gtaacgatac gttggcagat ttaccagaag 2696
 atttcaaaaa agtggttaaa gatgcagcag cgaaagccgc tgaatatcac actaaactct 2756
 tcgttgacgg tgagaacagc ttagttgaat t 2787

<210> 75
 <211> 158
 <212> PRT
 <213> Pasteurella multocida

<400> 75
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 Ser Ser Lys Leu Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu
 20 25 30
 Ile Arg Leu Ile Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val
 35 40 45
 Pro Ser Lys Ala Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met
 50 55 60
 Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg
 65 70 75 80
 Leu Thr Ile Pro Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe
 85 90 95

Lys Phe Ser Ile Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr
 100 105 110
 Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro
 115 120 125
 Leu Ser Thr Gly Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser
 130 135 140
 Lys Thr Cys Gly Cys Asp Ser Phe Asp Ile Leu Thr Pro Val
 145 150 155

<210> 76
 <211> 2787
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <221> CDS
 <222> (1949)..(2785)

<220>
 <223> yiaO

<400> 76
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 ggcgttgcaa tctgttggcg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
 tttgttccac caatatctaa tgctaaacag cgcatagggt ctccttctgt gatgacttat 240
 tttgccgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgca 300
 gatcctacgg tgacagagta agcaccaatc tcaattgcgg ttttcgccaa ttctgggggtg 360
 ttatagcgcc cttctgccat cactcggcag ccagcagcat tcaaactctt gactaactga 420
 taatccggtt cagctggaat ttcaccgcca gtataaccag acatggtgct accaataatt 480
 tctaccctta agttgtggca atacatccct tcttcaaaat tagaacaatc cgccatgggt 540
 aaacaaccta attctttgat tcgtttaata atgggttcac gtgtagttgg acggacgcga 600
 tcggtaccat caaaagcaat aatatcggcg cctgctgcgg ctaactcttc aatgtcttgt 660
 aaaaatgggc taatacgaac gggactgtca ggtaaatcgc gtttaacgat accaataatc 720
 ggtacattga cgacgttacg cgtggctttt aaattttcga tcccttcaat acgtaaccgc 780
 gcagcaccac cgataacgga tgcttgcgcc atggcggcaa caatttctgg cgagtccatt 840
 ggcccattat ctacgggctg gcaagatgcg attaagccat atttaatttg ttctaaaact 900
 tgcggatgtg atagttttga catattaact ccagtctaaa tttatcaaaa gaagattgac 960
 tccaatttgc atagggttaat cttagaatta aaaaataaca accaaaataa taaaaatttg 1020
 agatctttgt cgcataattta ttcataggga atagacagct taattttagt tatgatttgt 1080
 caatccttgc tattttttgt gtttgctggt ttgcgataca ctgttctaatt attgctttga 1140

gcacttgata accttgctca ttaaaatgta atccgtcggg acaaaggcgt aaatccagtt 1200
caccgttaga atcacaaaag tattttttgtg tttcaacgta agtcacgtct gacggacaat 1260
gttgtttttaa ataggtattg agcctgtgaa tttgtgcgtt agtgaccgta ttaatctgat 1320
tgaccgggtgt ggcttctaata aaaaagtagt gggacgtagg agaaatgggtg ttaggtgag 1380
tcagaatgtc atttaactat cgcgtgactt gcgccgggtga atacgtttct tccttacaaa 1440
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gaccaattaa gctgatattg gcaggtttgg aaaattccgc cattttgctc tgatagcgtt 1680
gataaatatc ctgatcactt agcatgtgtg gacctctatt ttgaaataaa acgctaagta 1740
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aattttgtga cgaacctatc atttatgaaa taaaacttca ttttctatat aaaaaatagt 1860
tttttcactt tagaatgcca aacgtgtgaa atttatttca tcatcatttt aacgtaatcc 1920
caacgtaacc aatagaggag aactcata atg aaa ttt aaa aaa cta cta ctt 1972
Met Lys Phe Lys Lys Leu Leu Leu
1 5

gca tct tta tgt tta ggt gtt tca gct tct gta ttt gca gca gat tac 2020
Ala Ser Leu Cys Leu Gly Val Ser Ala Ser Val Phe Ala Ala Asp Tyr
10 15 20

gat ctt aaa ttc ggt atg gtt gcg ggt cca agc tca aac gaa tat aaa 2068
Asp Leu Lys Phe Gly Met Val Ala Gly Pro Ser Ser Asn Glu Tyr Lys
25 30 35 40

gca gta gaa ttc ttt gcg aaa gaa gtg aaa gaa aaa tcc aat ggc aaa 2116
Ala Val Glu Phe Phe Ala Lys Glu Val Lys Glu Lys Ser Asn Gly Lys
45 50 55

att gat gtg gct att ttc cct agc tca cag tta ggt gat gac cgt gtg 2164
Ile Asp Val Ala Ile Phe Pro Ser Ser Gln Leu Gly Asp Asp Arg Val
60 65 70

atg att aaa caa tta aaa gac ggt gca tta gac ttt acg tta ggt gaa 2212
Met Ile Lys Gln Leu Lys Asp Gly Ala Leu Asp Phe Thr Leu Gly Glu
75 80 85

tca gca cgt ttc caa att tac ttc cca gaa gca gaa gta ttt gcg ttg 2260
Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu
90 95 100

cct tat atg att cct aat ttt gaa acc tct aaa aaa gcg ttg ctc gac 2308
Pro Tyr Met Ile Pro Asn Phe Glu Thr Ser Lys Lys Ala Leu Leu Asp
105 110 115 120

aca aaa ttt ggt caa ggt tta ttg aaa aaa att gat aaa gag tta aac 2356
Thr Lys Phe Gly Gln Gly Leu Leu Lys Lys Ile Asp Lys Glu Leu Asn
125 130 135

gta caa gtg tta tct gtg gcg tat aac ggt aca cgt caa aca act tct	2404
Val Gln Val Leu Ser Val Ala Tyr Asn Gly Thr Arg Gln Thr Thr Ser	
140 145 150	
aac cgt gca atc aac agc att gaa gac atg aaa ggg tta aaa tta cgt	2452
Asn Arg Ala Ile Asn Ser Ile Glu Asp Met Lys Gly Leu Lys Leu Arg	
155 160 165	
gta cct aac gcg gca acc aac ctt gct tat gca aaa tac gtg ggt gca	2500
Val Pro Asn Ala Ala Thr Asn Leu Ala Tyr Ala Lys Tyr Val Gly Ala	
170 175 180	
gcg cca aca cca atg gca ttc tct gaa gtt tac ctt gcg ctt caa aca	2548
Ala Pro Thr Pro Met Ala Phe Ser Glu Val Tyr Leu Ala Leu Gln Thr	
185 190 195 200	
aac tct gtg gat ggt caa gaa aac cca tta ccg aca atc caa gca caa	2596
Asn Ser Val Asp Gly Gln Glu Asn Pro Leu Pro Thr Ile Gln Ala Gln	
205 210 215	
aaa ttc tat gaa gta caa aaa tac tta gcg tta act aac cac atc tta	2644
Lys Phe Tyr Glu Val Gln Lys Tyr Leu Ala Leu Thr Asn His Ile Leu	
220 225 230	
aat gac caa ctt tac tta atc agt aac gat acg ttg gca gat tta cca	2692
Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro	
235 240 245	
gaa gat tta caa aaa gtg gtt aaa gat gca gca gcg aaa gcc gct gaa	2740
Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Lys Ala Ala Glu	
250 255 260	
tat cac act aaa ctc ttc gtt gac ggt gag aac agc tta gtt gaa tt	2787
Tyr His Thr Lys Leu Phe Val Asp Gly Glu Asn Ser Leu Val Glu	
265 270 275	

<210> 77

<211> 279

<212> PRT

<213> Pasteurella multocida

<400> 77

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Gly Pro Ser Ser Asn Glu Tyr Lys Ala Val Glu Phe Phe Ala Lys Glu	
35 40 45	
Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser	
50 55 60	
Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly	
65 70 75 80	
Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe	
85 90 95	
Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu	

100					105					110					
Thr	Ser	Lys	Lys	Ala	Leu	Leu	Asp	Thr	Lys	Phe	Gly	Gln	Gly	Leu	Leu
		115					120					125			
Lys	Lys	Ile	Asp	Lys	Glu	Leu	Asn	Val	Gln	Val	Leu	Ser	Val	Ala	Tyr
		130					135					140			
Asn	Gly	Thr	Arg	Gln	Thr	Thr	Ser	Asn	Arg	Ala	Ile	Asn	Ser	Ile	Glu
145							150					155			160
Asp	Met	Lys	Gly	Leu	Lys	Leu	Arg	Val	Pro	Asn	Ala	Ala	Thr	Asn	Leu
				165					170					175	
Ala	Tyr	Ala	Lys	Tyr	Val	Gly	Ala	Ala	Pro	Thr	Pro	Met	Ala	Phe	Ser
			180					185					190		
Glu	Val	Tyr	Leu	Ala	Leu	Gln	Thr	Asn	Ser	Val	Asp	Gly	Gln	Glu	Asn
		195					200					205			
Pro	Leu	Pro	Thr	Ile	Gln	Ala	Gln	Lys	Phe	Tyr	Glu	Val	Gln	Lys	Tyr
		210					215					220			
Leu	Ala	Leu	Thr	Asn	His	Ile	Leu	Asn	Asp	Gln	Leu	Tyr	Leu	Ile	Ser
225							230					235			240
Asn	Asp	Thr	Leu	Ala	Asp	Leu	Pro	Glu	Asp	Leu	Gln	Lys	Val	Val	Lys
				245					250					255	
Asp	Ala	Ala	Ala	Lys	Ala	Ala	Glu	Tyr	His	Thr	Lys	Leu	Phe	Val	Asp
			260					265					270		
Gly	Glu	Asn	Ser	Leu	Val	Glu									
		275													

<210> 78
 <211> 2590
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (908)..(1294)

<220>
 <223> yigF

<400> 78
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 aaagtgcggg ggcaattcgt tttattgagc aagtggacga gaaattgatt ttccgcagcg 180
 gtggcgggat tacgatctta agcgagctag aagacgagta ccaagaattg atccaaaaag 240
 tgtatgtacc agtaggataa gcgatgacat ttcctttatt tgagacgacg gctattgtga 300
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 ttacggcgga gaaaggagcg aaagtacagg atcttgcgaa aattattcag attccgacct 420

cacttgaaca cactcaacat gcgccgataa tccgttgctcg gattgattac aatcagcaag 480
actgtgacgt gcattatctt ccctatcaac gcaaaattta ccgcactttt cagcctgtca 540
tttgcgatga aattaactat gatctgaaat atgctgatcg ggcattatta aatcagttat 600
ttgctcagcg tagggattgt gatgagatta tgattatcaa acacggcaag gtgacggatt 660
gcagtattgg taatctggtg tttcgccaag gtgagcaatg gttcacgcca gatagcccgt 720
tattttacgg cacacaacga gcctgggttat tacaacaagg caaaattcaa gcccgttcca 780
tcttattgca agagatcgca caatttgaag aaattcgggt aattaatgca ctaaaccgc 840
tgtaaatttt ccttgaacag cgtaaaataa aacaactttt tcagtcagat aaaaggagat 900

aaacgac atg acg aaa gta att cat act gac aat gca cca gcc gcc att 949
Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile
1 5 10

ggg cct tat gta caa gcg gta gat tta ggt aat atg ctg tta acc tct 997
Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser
15 20 25 30

ggg caa att cca gtg aat cca aaa acc ggt gaa gtg cca gcg gat atc 1045
Gly Gln Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile
35 40 45

gta gca caa gca cgt caa tcg tta gaa aac gtg aaa gcg att gtg gaa 1093
Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu
50 55 60

caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg 1141
Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val
65 70 75

aaa gat tta aat gac ttt gca gcg gtc aat gcg gag tat gaa cgt ttc 1189
Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe
80 85 90

ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa 1237
Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu
95 100 105 110

gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct 1285
Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala
115 120 125

gta aaa gcc taatgaatag cttgcattta tcttagtcgt agcaaaacaa 1334
Val Lys Ala

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Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala Ser Leu Ile				
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Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys Pro Thr Gly				
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Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln Gly Leu Arg				
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Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys Ala Ile Thr				
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Ser	Leu	Ile	Ser	Pro	Met	Glu	Ala	Gly	Thr	Pro	Tyr	Phe	Ile	Ala	Arg
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Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr
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Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro Ser Ser Ser
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<223> Description of Artificial Sequence: primer

<400> 92

tacccattct aaccaagc

18

<210> 93

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 93

tacctacaac ctcaagctt

19

<210> 94

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 94
taccattctt aaccaagctt

20

<210> 95
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 95
ggcagagcat tacgctgac

19

<210> 96
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 96
gtaccggcca ggcggccacg cgtattc

27

<210> 97
<211> 531
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>

<223> atpG

<400> 97
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cgtgagatct caagtaacgg gattaggcga taatccggaa atggaacgta tcgtgggcgc 120
agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcggttt acgtcgctta 180
caaccgtttt gaaaatacga tgtcacaaaa acctgttatt gcacagttac ttccgttacc 240
taaactagat gacgatgaat tagatacga aggttcatgg gattatattt atgaaccgaa 300
tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360
agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420
agataatgcg ggtacattaa tcgatgaatt acaattagt tataacaaag ctgcgcaagc 480
aagcattaca aatgaattaa acgaaattgt tgcgggtgcc gcagcaattt a 531

<210> 98
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 98
tctccattcc cttgctgcgg caccc 25

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 99
ggattacagc cggatccggg 20

<210> 100
<211> 1034
<212> DNA
<213> Pasteurella multocida

<220>
<223> cap5E

<220>
<221> CDS
<222> (1)..(1032)

<400> 100
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Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe
1 5 10 15

ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96
Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile
20 25 30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa 144
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys
35 40 45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr
50 55 60

gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct 240
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala
65 70 75 80

gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca 288
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala
85 90 95

gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc 336
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile
100 105 110

caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg 384
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val
115 120 125

tac cca att aat gcg atg ggc att tct aaa gca atg atg gaa aaa gtc 432
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val

130

135

140

atc	atc	gca	aaa	tcg	cgt	aac	cta	gaa	ggc	aca	cca	acg	aca	atc	tgt	480
Ile	Ile	Ala	Lys	Ser	Arg	Asn	Leu	Glu	Gly	Thr	Pro	Thr	Thr	Ile	Cys	
145					150				155						160	
tgt	act	cgc	tat	ggc	aat	gtc	atg	gca	tcg	cgt	ggg	tcg	gtt	atc	cca	528
Cys	Thr	Arg	Tyr	Gly	Asn	Val	Met	Ala	Ser	Arg	Gly	Ser	Val	Ile	Pro	
				165					170					175		
tta	ttt	gtc	gat	caa	ata	cgt	caa	ggc	aag	cct	ttt	act	att	act	gat	576
Leu	Phe	Val	Asp	Gln	Ile	Arg	Gln	Gly	Lys	Pro	Phe	Thr	Ile	Thr	Asp	
			180					185					190			
cct	gag	atg	aca	cgc	ttt	atg	atg	aca	ttg	gaa	gat	gct	gtg	gat	tta	624
Pro	Glu	Met	Thr	Arg	Phe	Met	Met	Thr	Leu	Glu	Asp	Ala	Val	Asp	Leu	
		195					200					205				
gtc	cta	tat	gca	ttt	aaa	aat	ggg	caa	aat	ggg	gat	gtt	ttt	gta	caa	672
Val	Leu	Tyr	Ala	Phe	Lys	Asn	Gly	Gln	Asn	Gly	Asp	Val	Phe	Val	Gln	
	210					215					220					
aaa	gcc	ccc	gca	gca	acc	att	ggg	acc	ctt	gcc	aaa	gca	att	acc	gaa	720
Lys	Ala	Pro	Ala	Ala	Thr	Ile	Gly	Thr	Leu	Ala	Lys	Ala	Ile	Thr	Glu	
225					230				235						240	
tta	tta	tct	gtc	cca	aat	cac	cct	att	tcc	att	ata	ggg	acg	cgt	cat	768
Leu	Leu	Ser	Val	Pro	Asn	His	Pro	Ile	Ser	Ile	Ile	Gly	Thr	Arg	His	
				245				250						255		
gga	gag	aaa	gca	ttc	gaa	gct	tta	tta	agc	cgt	gaa	gaa	atg	gtt	cat	816
Gly	Glu	Lys	Ala	Phe	Glu	Ala	Leu	Leu	Ser	Arg	Glu	Glu	Met	Val	His	
			260				265						270			
gca	att	aat	gaa	ggg	aat	tat	tat	cgc	atc	cca	gcc	gat	caa	cgc	agt	864
Ala	Ile	Asn	Glu	Gly	Asn	Tyr	Tyr	Arg	Ile	Pro	Ala	Asp	Gln	Arg	Ser	
		275					280					285				
tta	aat	tac	agt	aaa	tat	gtc	gaa	aaa	ggg	gaa	cca	aaa	att	acc	gaa	912
Leu	Asn	Tyr	Ser	Lys	Tyr	Val	Glu	Lys	Gly	Glu	Pro	Lys	Ile	Thr	Glu	
	290					295					300					
gtc	acc	gac	tac	aac	tca	cat	aat	act	gag	cgt	ttg	act	gtc	aag	gaa	960
Val	Thr	Asp	Tyr	Asn	Ser	His	Asn	Thr	Glu	Arg	Leu	Thr	Val	Lys	Glu	
305					310				315						320	
atg	aag	cag	tta	ctg	ctt	aaa	ctt	gaa	ttc	ata	cag	aaa	atg	att	gag	1008
Met	Lys	Gln	Leu	Leu	Leu	Lys	Leu	Glu	Phe	Ile	Gln	Lys	Met	Ile	Glu	
				325				330						335		
ggg	gaa	tac	atc	tca	ccg	gag	gta	ta								1034
Gly	Glu	Tyr	Ile	Ser	Pro	Glu	Val									
				340												

<210> 101

<211> 344

<212> PRT

<213> Pasteurella multocida

<400> 101

Met	Phe	Lys	Asn	Lys	Thr	Leu	Leu	Ile	Thr	Gly	Gly	Thr	Gly	Ser	Phe	1	5	10	15
Gly	Asn	Ala	Val	Leu	Lys	Arg	Phe	Leu	Glu	Thr	Asp	Ile	Arg	Glu	Ile	20	25	30	
Arg	Val	Phe	Ser	Arg	Asp	Glu	Lys	Lys	Gln	Asp	Asp	Met	Arg	Lys	Lys	35	40	45	
Tyr	Asn	Asp	Ala	Lys	Leu	Lys	Phe	Tyr	Ile	Gly	Asp	Val	Arg	Asp	Tyr	50	55	60	
Asp	Ser	Ile	Leu	Asn	Ala	Ser	Arg	Gly	Val	Asp	Tyr	Ile	Tyr	His	Ala	65	70	75	80
Ala	Ala	Leu	Lys	Gln	Val	Pro	Ser	Cys	Glu	Phe	Tyr	Pro	Leu	Glu	Ala	85	90	95	
Val	Lys	Thr	Asn	Ile	Leu	Gly	Thr	Ala	Asn	Val	Leu	Glu	Ala	Ala	Ile	100	105	110	
Gln	Asn	Gln	Ile	Lys	Arg	Val	Val	Cys	Leu	Ser	Thr	Asp	Lys	Ala	Val	115	120	125	
Tyr	Pro	Ile	Asn	Ala	Met	Gly	Ile	Ser	Lys	Ala	Met	Met	Glu	Lys	Val	130	135	140	
Ile	Ile	Ala	Lys	Ser	Arg	Asn	Leu	Glu	Gly	Thr	Pro	Thr	Thr	Ile	Cys	145	150	155	160
Cys	Thr	Arg	Tyr	Gly	Asn	Val	Met	Ala	Ser	Arg	Gly	Ser	Val	Ile	Pro	165	170	175	
Leu	Phe	Val	Asp	Gln	Ile	Arg	Gln	Gly	Lys	Pro	Phe	Thr	Ile	Thr	Asp	180	185	190	
Pro	Glu	Met	Thr	Arg	Phe	Met	Met	Thr	Leu	Glu	Asp	Ala	Val	Asp	Leu	195	200	205	
Val	Leu	Tyr	Ala	Phe	Lys	Asn	Gly	Gln	Asn	Gly	Asp	Val	Phe	Val	Gln	210	215	220	
Lys	Ala	Pro	Ala	Ala	Thr	Ile	Gly	Thr	Leu	Ala	Lys	Ala	Ile	Thr	Glu	225	230	235	240
Leu	Leu	Ser	Val	Pro	Asn	His	Pro	Ile	Ser	Ile	Ile	Gly	Thr	Arg	His	245	250	255	
Gly	Glu	Lys	Ala	Phe	Glu	Ala	Leu	Leu	Ser	Arg	Glu	Glu	Met	Val	His	260	265	270	
Ala	Ile	Asn	Glu	Gly	Asn	Tyr	Tyr	Arg	Ile	Pro	Ala	Asp	Gln	Arg	Ser	275	280	285	
Leu	Asn	Tyr	Ser	Lys	Tyr	Val	Glu	Lys	Gly	Glu	Pro	Lys	Ile	Thr	Glu	290	295	300	
Val	Thr	Asp	Tyr	Asn	Ser	His	Asn	Thr	Glu	Arg	Leu	Thr	Val	Lys	Glu	305	310	315	320
Met	Lys	Gln	Leu	Leu	Leu	Lys	Leu	Glu	Phe	Ile	Gln	Lys	Met	Ile	Glu	325	330	335	

Gly Glu Tyr Ile Ser Pro Glu Val
340

<210> 102
<211> 4931
<212> DNA
<213> Pasteurella multocida

<220>
<223> fhaB2

<220>
<221> CDS
<222> (1)..(4929)

<220>
<221> misc_feature
<222> 4894
<223> n = A or T or G or C

<400> 102
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Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
1 5 10 15
ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca 96
Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser
20 25 30
tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt 144
Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
35 40 45
cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg 192
Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
50 55 60
ttc aat cct gtt tcg tat gca atg caa ttg act tgg aaa cag ctt tct 240
Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
65 70 75 80
att tta ttt tta act gtg att tct gtt cct gtt ttg gct gag gga aaa 288
Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
85 90 95
ggg gat gaa aga aat caa tta aca gtg att gat aat agc gat cat att 336
Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
100 105 110
aaa tta gat gca tct aat ctt gct ggt aat gat aaa aca aaa atc tat 384
Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
115 120 125
caa gca gaa aat aaa gtt ctg gtt att gat att gct aaa cca aat ggg 432
Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
130 135 140
aaa ggg att tca gat aac cgt ttt gaa aaa ttt aat att cca aat agc 480
Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
145 150 155 160
gcg gtg ttt aat aat aat ggg act gaa gcg cag gca aga tca aca tta 528

Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu	165	170	175	
att ggt tac att ccg caa aat caa aat tta agg gga ggg aaa gaa gct	576			
Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala	180	185	190	
gat gtt ata tta aat caa gtg aca ggt cct caa gaa agt aaa att gtt	624			
Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val	195	200	205	
ggc gcg ctt gaa gta tta ggt aaa aaa gct gat atc gtc att gca aac	672			
Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn	210	215	220	
caa aat ggt att acc tta aat ggt gta aga aca ata aat tca gat cgt	720			
Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg	225	230	235	240
ttt gtt gcc act acg agt gag ctt ata gat ccg aat cag atg atg tta	768			
Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu	245	250	255	
aag gtt aca aaa gga aat gtg atc att gat att gat ggt ttt tcg aca	816			
Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr	260	265	270	
gat gga tta aag tat tta gat att att gct aaa aaa att gaa caa aag	864			
Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys	275	280	285	
caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act	912			
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	290	295	300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa	960			
Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	305	310	315	320
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga	1008			
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	325	330	335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca	1056			
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	340	345	350	
gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat	1104			
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	355	360	365	
gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg	1152			
Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr	370	375	380	
att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa	1200			
Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys	385	390	395	400
aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg	1248			
Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr	405	410	415	

aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa	1296
Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys	
420 425 430	
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt	1344
Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly	
435 440 445	
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat	1392
Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp	
450 455 460	
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag	1440
Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu	
465 470 475 480	
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct	1488
Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala	
485 490 495	
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att	1536
Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile	
500 505 510	
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc	1584
Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg	
515 520 525	
ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc	1632
Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser	
530 535 540	
ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa	1680
Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu	
545 550 555 560	
agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta	1728
Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu	
565 570 575	
aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac	1776
Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn	
580 585 590	
gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct	1824
Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala	
595 600 605	
aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca	1872
Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr	
610 615 620	
ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att	1920
Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile	
625 630 635 640	
tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act	1968
Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr	
645 650 655	
gct aaa tca acg gaa gaa ggt atg gga aat att gtt aac caa gaa aac	2016
Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn	

660						665						670						
ggt	tta	ttc	cat	aca	ctc	ggt	aat	atg	atg	tta	gaa	gca	gag	cgt	tct	2064		
Gly	Leu	Phe	His	Thr	Leu	Gly	Asn	Met	Met	Leu	Glu	Ala	Glu	Arg	Ser			
		675					680					685						
ggt	tat	aat	att	ggc	gat	att	tat	gcg	agt	aaa	aaa	tta	aca	ggt	cat	2112		
Val	Tyr	Asn	Ile	Gly	Asp	Ile	Tyr	Ala	Ser	Lys	Lys	Leu	Thr	Val	His			
	690					695					700							
act	cat	aat	ttg	att	aat	gat	gtg	cgt	tta	tct	ggc	aat	gtg	agt	tat	2160		
Thr	His	Asn	Leu	Ile	Asn	Asp	Val	Arg	Leu	Ser	Gly	Asn	Val	Ser	Tyr			
705					710					715					720			
aag	cct	atc	ggg	tca	agt	cgt	gat	tat	gat	atc	agt	cgt	ggt	gcg	gta	2208		
Lys	Pro	Ile	Gly	Ser	Ser	Arg	Asp	Tyr	Asp	Ile	Ser	Arg	Val	Ala	Val			
				725					730					735				
cat	ggt	tggt	cac	aat	aat	ggt	tat	aag	ctc	aac	tta	aat	ctg	caa	gaa	2256		
His	Gly	Trp	His	Asn	Asn	Val	Tyr	Lys	Leu	Asn	Leu	Asn	Leu	Gln	Glu			
			740					745					750					
caa	gat	aaa	acc	gat	att	aaa	ggt	gtg	aaa	atg	ggg	gct	atc	cgt	tct	2304		
Gln	Asp	Lys	Thr	Asp	Ile	Lys	Val	Val	Lys	Met	Gly	Ala	Ile	Arg	Ser			
		755					760					765						
gat	ggt	gat	ttt	gac	ttt	aag	gga	ata	aag	gcg	aca	tca	tca	gaa	tca	2352		
Asp	Gly	Asp	Phe	Asp	Phe	Lys	Gly	Ile	Lys	Ala	Thr	Ser	Ser	Glu	Ser			
	770					775					780							
aaa	ccg	cag	tta	att	aat	cat	gga	tta	att	aat	gtc	aaa	gga	aca	ttt	2400		
Lys	Pro	Gln	Leu	Ile	Asn	His	Gly	Leu	Ile	Asn	Val	Lys	Gly	Thr	Phe			
785					790					795					800			
aat	gcg	gaa	gct	gat	caa	gtg	gtg	aac	caa	atg	aaa	gcg	ttt	aac	caa	2448		
Asn	Ala	Glu	Ala	Asp	Gln	Val	Val	Asn	Gln	Met	Lys	Ala	Phe	Asn	Gln			
				805					810					815				
aat	gca	tta	gca	agc	gtg	ttt	aag	aat	cca	gcg	aaa	atc	acg	atg	tac	2496		
Asn	Ala	Leu	Ala	Ser	Val	Phe	Lys	Asn	Pro	Ala	Lys	Ile	Thr	Met	Tyr			
			820					825					830					
tat	caa	cca	ctt	act	cgt	tat	att	tggt	aca	cca	tta	tcg	ggg	aat	gca	2544		
Tyr	Gln	Pro	Leu	Thr	Arg	Tyr	Ile	Trp	Thr	Pro	Leu	Ser	Gly	Asn	Ala			
		835					840					845						
tcg	cgt	gaa	ttt	aac	aat	tta	gag	tct	ttc	ctc	gat	gcc	ttg	ttt	ggc	2592		
Ser	Arg	Glu	Phe	Asn	Asn	Leu	Glu	Ser	Phe	Leu	Asp	Ala	Leu	Phe	Gly			
	850					855					860							
tca	aca	aca	atc	tta	aaa	tca	agt	ttc	tat	agt	acg	gaa	aat	ttt	agt	2640		
Ser	Thr	Thr	Ile	Leu	Lys	Ser	Ser	Phe	Tyr	Ser	Thr	Glu	Asn	Phe	Ser			
865					870					875					880			
gct	tat	cag	ctt	cta	tct	cat	att	cag	cat	tca	cca	atg	tac	caa	aaa	2688		
Ala	Tyr	Gln	Leu	Leu	Ser	His	Ile	Gln	His	Ser	Pro	Met	Tyr	Gln	Lys			
				885					890					895				
gcg	atg	gca	caa	gtg	ttt	ggg	gca	gag	tggt	cat	agt	aaa	tcc	tat	gat	2736		
Ala	Met	Ala	Gln	Val	Phe	Gly	Ala	Glu	Trp	His	Ser	Lys	Ser	Tyr	Asp			
			900					905					910					

gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc	2784
Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe	
915 920 925	
att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa	2832
Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu	
930 935 940	
ggg aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag	2880
Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys	
945 950 955 960	
ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca	2928
Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser	
965 970 975	
gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac	2976
Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp	
980 985 990	
ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta	3024
Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu	
995 1000 1005	
ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct cct att	3072
Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile	
1010 1015 1020	
gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc	3120
Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser	
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cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat gag tct	3168
His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser	
1045 1050 1055	
gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa gag atg	3216
Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met	
1060 1065 1070	
ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca	3264
Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro	
1075 1080 1085	
cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt	3312
Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe	
1090 1095 1100	
gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag	3360
Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu	
1105 1110 1115 1120	
ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta	3408
Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu	
1125 1130 1135	
gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa	3456
Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys	
1140 1145 1150	
gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag	3504
Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu	

1155	1160	1165	
tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg 1170 1175 1180			3552
ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa cgt gtt Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val 1185 1190 1195 1200			3600
gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa att gct Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala 1205 1210 1215			3648
aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg 1220 1225 1230			3696
cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag aag aaa Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys 1235 1240 1245			3744
caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct gaa cag Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln 1250 1255 1260			3792
aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac att gaa Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu 1265 1270 1275 1280			3840
caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag gca tca Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser 1285 1290 1295			3888
aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa gtg gaa Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu 1300 1305 1310			3936
act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp 1315 1320 1325			3984
tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat aca aaa Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys 1330 1335 1340			4032
ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln 1345 1350 1355 1360			4080
gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt aac caa Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln 1365 1370 1375			4128
aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn 1380 1385 1390			4176
tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu 1395 1400 1405			4224

act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg tat gtc Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val 1410 1415 1420	4272
aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt tat ttc Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe 1425 1430 1435 1440	4320
gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta ggc act Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr 1445 1450 1455	4368
ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat gtg gtg Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val 1460 1465 1470	4416
aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn 1475 1480 1485	4464
aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca cgt tta Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu 1490 1495 1500	4512
gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp 1505 1510 1515 1520	4560
gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His 1525 1530 1535	4608
tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser 1540 1545 1550	4656
gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg aat ctc Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu 1555 1560 1565	4704
aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc tcg ccg Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro 1570 1575 1580	4752
agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa gtc cca Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro 1585 1590 1595 1600	4800
ctt tta ggc gtg tcc gtc tcc atc cag ttt att cag agc ata cta gtg Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val 1605 1610 1615	4848
agg caa ctt caa gag gga tca atc ttc gaa gta ggg cac tta cat ntt Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa 1620 1625 1630	4896
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<400> 103

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			20					25					30		
Ser	Asp	Ser	Thr	Ser	Thr	Ser	Glu	Gln	Val	Glu	Glu	Glu	Pro	Phe	Leu
	35						40					45			
Leu	Glu	Gln	Tyr	Ser	Leu	Ser	Ser	Val	Ser	Leu	Leu	Val	Lys	Ser	Thr
	50					55					60				
Phe	Asn	Pro	Val	Ser	Tyr	Ala	Met	Gln	Leu	Thr	Trp	Lys	Gln	Leu	Ser
65					70					75					80
Ile	Leu	Phe	Leu	Thr	Val	Ile	Ser	Val	Pro	Val	Leu	Ala	Glu	Gly	Lys
				85					90					95	
Gly	Asp	Glu	Arg	Asn	Gln	Leu	Thr	Val	Ile	Asp	Asn	Ser	Asp	His	Ile
			100					105					110		
Lys	Leu	Asp	Ala	Ser	Asn	Leu	Ala	Gly	Asn	Asp	Lys	Thr	Lys	Ile	Tyr
	115						120					125			
Gln	Ala	Glu	Asn	Lys	Val	Leu	Val	Ile	Asp	Ile	Ala	Lys	Pro	Asn	Gly
	130					135					140				
Lys	Gly	Ile	Ser	Asp	Asn	Arg	Phe	Glu	Lys	Phe	Asn	Ile	Pro	Asn	Ser
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Ala	Val	Phe	Asn	Asn	Asn	Gly	Thr	Glu	Ala	Gln	Ala	Arg	Ser	Thr	Leu
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Ile	Gly	Tyr	Ile	Pro	Gln	Asn	Gln	Asn	Leu	Arg	Gly	Gly	Lys	Glu	Ala
			180					185					190		
Asp	Val	Ile	Leu	Asn	Gln	Val	Thr	Gly	Pro	Gln	Glu	Ser	Lys	Ile	Val
	195						200					205			
Gly	Ala	Leu	Glu	Val	Leu	Gly	Lys	Lys	Ala	Asp	Ile	Val	Ile	Ala	Asn
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Gln	Asn	Gly	Ile	Thr	Leu	Asn	Gly	Val	Arg	Thr	Ile	Asn	Ser	Asp	Arg
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Phe	Val	Ala	Thr	Thr	Ser	Glu	Leu	Ile	Asp	Pro	Asn	Gln	Met	Met	Leu
				245					250					255	
Lys	Val	Thr	Lys	Gly	Asn	Val	Ile	Ile	Asp	Ile	Asp	Gly	Phe	Ser	Thr
			260				265						270		
Asp	Gly	Leu	Lys	Tyr	Leu	Asp	Ile	Ile	Ala	Lys	Lys	Ile	Glu	Gln	Lys

275					280					285					
Gln	Ser	Ile	Thr	Ser	Gly	Asp	Asn	Ser	Glu	Ala	Lys	Thr	Asp	Val	Thr
290						295					300				
Leu	Ile	Ala	Gly	Ser	Ser	Glu	Tyr	Asp	Leu	Ser	Lys	His	Glu	Leu	Lys
305					310					315					320
Lys	Thr	Ser	Gly	Glu	Asn	Val	Ser	Asn	Asp	Val	Ile	Ala	Ile	Thr	Gly
				325					330					335	
Ser	Ser	Thr	Gly	Ala	Met	His	Gly	Lys	Asn	Ile	Lys	Leu	Ile	Val	Thr
			340					345					350		
Asp	Lys	Gly	Ala	Gly	Val	Lys	His	Asp	Gly	Ile	Ile	Leu	Ser	Glu	Asn
		355					360					365			
Asp	Ile	Gln	Ile	Glu	Met	Asn	Glu	Gly	Asp	Leu	Glu	Leu	Gly	Asn	Thr
	370					375					380				
Ile	Gln	Gln	Thr	Val	Val	Lys	Lys	Asp	Arg	Asn	Ile	Arg	Ala	Lys	Lys
385					390					395					400
Lys	Ile	Glu	Val	Lys	Asn	Ala	Asn	Arg	Val	Phe	Val	Gly	Ser	Gln	Thr
				405					410					415	
Lys	Ser	Asp	Glu	Ile	Ser	Leu	Glu	Ala	Lys	Gln	Val	Lys	Ile	Arg	Lys
			420					425					430		
Asn	Ala	Glu	Ile	Arg	Ser	Thr	Thr	Gln	Ala	Lys	Ile	Val	Ala	Lys	Gly
		435					440					445			
Ala	Leu	Ser	Ile	Glu	Gln	Asn	Ala	Lys	Leu	Val	Ala	Lys	Lys	Ile	Asp
	450					455					460				
Val	Ala	Thr	Glu	Thr	Leu	Thr	Asn	Ala	Gly	Arg	Ile	Tyr	Gly	Arg	Glu
465					470					475					480
Val	Lys	Leu	Asp	Thr	Asn	Asn	Leu	Ile	Asn	Asp	Lys	Glu	Ile	Tyr	Ala
				485					490					495	
Glu	Arg	Lys	Leu	Ser	Ile	Leu	Thr	Lys	Gly	Lys	Asp	Leu	Glu	Ile	Ile
			500					505					510		
Gln	Asp	Arg	Tyr	Leu	Ser	Pro	Leu	Met	Arg	Val	Lys	Ser	Ser	Val	Arg
		515					520					525			
Phe	Leu	Gly	Ser	Pro	Phe	Phe	Ser	Ile	Ser	Pro	Ser	Met	Leu	Ala	Ser
	530					535					540				
Leu	Ser	Ala	Gln	Phe	Lys	Pro	Gly	Phe	Val	Asn	Lys	Gly	Leu	Ile	Glu
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Ser	Ala	Gly	Ser	Ala	Glu	Leu	Thr	Phe	Lys	Glu	Lys	Thr	Ser	Phe	Leu
				565					570					575	
Thr	Glu	Gly	Asn	Asn	Phe	Ile	Arg	Ala	Lys	Asp	Ala	Leu	Thr	Ile	Asn
			580					585					590		
Ala	Gln	Asn	Ile	Glu	Ile	Asp	Lys	Asn	Gln	Asp	Ile	Gln	Leu	Gly	Ala
		595					600					605			

Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
 610 615 620
 Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
 625 630 635 640
 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
 645 650 655
 Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
 660 665 670
 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
 675 680 685
 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
 690 695 700
 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
 705 710 715 720
 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
 725 730 735
 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
 740 745 750
 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
 755 760 765
 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
 770 775 780
 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
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 Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
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 Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
 820 825 830
 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
 835 840 845
 Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly
 850 855 860
 Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser
 865 870 875 880
 Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
 885 890 895
 Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
 900 905 910
 Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe
 915 920 925
 Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
 930 935 940

Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
 945 950 955 960
 Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
 965 970 975
 Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp
 980 985 990
 Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
 995 1000 1005
 Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile
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 Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
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 His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser
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 Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
 1060 1065 1070
 Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
 1075 1080 1085
 Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
 1090 1095 1100
 Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
 1105 1110 1115 1120
 Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
 1125 1130 1135
 Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
 1140 1145 1150
 Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
 1155 1160 1165
 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
 1170 1175 1180
 Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
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 1220 1225 1230
 Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Lys Lys
 1235 1240 1245
 Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
 1250 1255 1260
 Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
 1265 1270 1275 1280

Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
 1285 1290 1295
 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
 1300 1305 1310
 Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp
 1315 1320 1325
 Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
 1330 1335 1340
 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
 1345 1350 1355 1360
 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
 1365 1370 1375
 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
 1380 1385 1390
 Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
 1395 1400 1405
 Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
 1410 1415 1420
 Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
 1425 1430 1435 1440
 Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
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 Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
 1460 1465 1470
 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
 1475 1480 1485
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 1490 1495 1500
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 Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
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 1540 1545 1550
 Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
 1555 1560 1565
 Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
 1570 1575 1580
 Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
 1585 1590 1595 1600
 Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
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Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
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Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
 1635 1640

<210> 104
 <211> 2009
 <212> DNA
 <213> Pasteurella multocida

<220>
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<220>
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 Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
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 cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg 144
 Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45
 ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg 192
 Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60
 tta ggt gga acc gtg gag ttt acc aca aaa gat att gag gac ttt gtc 240
 Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80
 gaa cct ggt cgc cat ttg ggc ttt ttg tct aaa acc ggc tat act tca 288
 Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
 85 90 95
 aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa 336
 Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
 100 105 110
 cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca 384
 His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
 115 120 125
 atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa 432
 Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
 130 135 140
 ccc aat ccg ctc aac tac tat act aca tca tgg tta acg aaa gtc ggt 480
 Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
 145 150 155 160
 tac gat att aat aac act cat cgt ttt aca ctg ttt tta gaa gat cgc 528

Tyr	Asp	Ile	Asn	Asn	Thr	His	Arg	Phe	Thr	Leu	Phe	Leu	Glu	Asp	Arg		
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Arg	Glu	Lys	Lys	Leu	Thr	Glu	Glu	Lys	Thr	Leu	Gly	Leu	Ser	Asp	Ala		
			180					185					190				
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Val	Arg	Phe	Ala	Asn	Asp	Gln	Thr	Pro	Tyr	Leu	Arg	Tyr	Gly	Ile	Glu		
		195					200					205					
tat	cga	tat	aac	ggc	ttg	tct	tgg	ttg	gaa	acg	gta	aag	ctt	ttt	ttg	672	
Tyr	Arg	Tyr	Asn	Gly	Leu	Ser	Trp	Leu	Glu	Thr	Val	Lys	Leu	Phe	Leu		
	210					215					220						
gca	aag	cag	aaa	atc	gaa	caa	cgt	tct	gct	ctc	caa	gag	ttt	gat	att	720	
Ala	Lys	Gln	Lys	Ile	Glu	Gln	Arg	Ser	Ala	Leu	Gln	Glu	Phe	Asp	Ile		
225					230					235				240			
aat	aat	agg	aat	aaa	ttg	gat	tcg	act	atg	tcg	ttt	gta	tat	tta	caa	768	
Asn	Asn	Arg	Asn	Lys	Leu	Asp	Ser	Thr	Met	Ser	Phe	Val	Tyr	Leu	Gln		
				245				250						255			
aga	cag	aat	ata	gct	cgg	gga	gaa	ttt	tca	acg	agt	cct	tta	tat	tgg	816	
Arg	Gln	Asn	Ile	Ala	Arg	Gly	Glu	Phe	Ser	Thr	Ser	Pro	Leu	Tyr	Trp		
			260					265					270				
ggg	ccg	agt	cgc	cat	cgt	tta	tct	gcg	aaa	ttc	gaa	ttt	cgt	gat	aag	864	
Gly	Pro	Ser	Arg	His	Arg	Leu	Ser	Ala	Lys	Phe	Glu	Phe	Arg	Asp	Lys		
		275					280					285					
ttt	tta	gaa	aat	atg	aat	aag	cat	ttt	acg	ttt	cgg	ccg	tgg	caa	atc	912	
Phe	Leu	Glu	Asn	Met	Asn	Lys	His	Phe	Thr	Phe	Arg	Pro	Trp	Gln	Ile		
	290					295					300						
aat	aga	ttc	aga	caa	caa	ggt	cga	aat	aac	tat	aca	gaa	gtg	ttt	ccc	960	
Asn	Arg	Phe	Arg	Gln	Gln	Gly	Arg	Asn	Asn	Tyr	Thr	Glu	Val	Phe	Pro		
305					310					315					320		
gtt	aaa	tcc	cga	gag	ttt	tct	ttt	tct	ctt	atg	gac	gac	att	aag	att	1008	
Val	Lys	Ser	Arg	Glu	Phe	Ser	Phe	Ser	Leu	Met	Asp	Asp	Ile	Lys	Ile		
				325					330					335			
ggc	gaa	ttg	cta	cat	ctc	gga	ttg	ggc	ggt	cgg	tgg	gat	cac	tat	aac	1056	
Gly	Glu	Leu	Leu	His	Leu	Gly	Leu	Gly	Gly	Arg	Trp	Asp	His	Tyr	Asn		
			340					345					350				
tat	aag	cca	tta	tta	aat	tct	cag	cat	aat	atc	aac	agg	aca	cag	aga	1104	
Tyr	Lys	Pro	Leu	Leu	Asn	Ser	Gln	His	Asn	Ile	Asn	Arg	Thr	Gln	Arg		
		355					360					365					
tta	cct	tat	cca	aaa	aca	tca	tcc	aaa	ttt	tcg	tat	caa	ttg	agt	tta	1152	
Leu	Pro	Tyr	Pro	Lys	Thr	Ser	Ser	Lys	Phe	Ser	Tyr	Gln	Leu	Ser	Leu		
	370					375					380						
gag	tat	caa	tta	cat	cca	tca	cat	caa	att	gca	tac	cgt	tta	agt	acc	1200	
Glu	Tyr	Gln	Leu	His	Pro	Ser	His	Gln	Ile	Ala	Tyr	Arg	Leu	Ser	Thr		
385					390					395					400		
ggt	ttt	agg	gtt	ccc	cgt	gtt	gaa	gat	ctt	tat	ttt	gaa	gac	cga	gga	1248	
Gly	Phe	Arg	Val	Pro	Arg	Val	Glu	Asp	Leu	Tyr	Phe	Glu	Asp	Arg	Gly		
				405					410					415			

aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act	1296
Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr	
420 425 430	
gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat	1344
Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His	
435 440 445	
ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa	1392
Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu	
450 455 460	
cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat	1440
Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr	
465 470 475 480	
gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa	1488
Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu	
485 490 495	
gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tcg gca	1536
Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala	
500 505 510	
ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc	1584
Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser	
515 520 525	
aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg	1632
Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp	
530 535 540	
aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt	1680
Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser	
545 550 555 560	
ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa	1728
Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu	
565 570 575	
acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta	1776
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu	
580 585 590	
agt cca tcc tac ttt gtt gtt gat ttt acg ggg caa gtt aac ctc agt	1824
Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser	
595 600 605	
aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat	1872
Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp	
610 615 620	
tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act	1920
Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr	
625 630 635 640	
tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca	1968
Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala	
645 650 655	
cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta	2009
Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe	

<210> 105

<211> 669

<212> PRT

<213> *Pasteurella multocida*

<400> 105

Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
 1 5 10 15

Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
 20 25 30

Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45

Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
 85 90 95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
 100 105 110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
 115 120 125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
 130 135 140

Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
 145 150 155 160

Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
 165 170 175

Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
 180 185 190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
 195 200 205

Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
 210 215 220

Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
 225 230 235 240

Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
 245 250 255

Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
 260 265 270

Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
 275 280 285

Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
290 295 300
Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
305 310 315 320
Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
325 330 335
Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
340 345 350
Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
355 360 365
Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
370 375 380
Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
385 390 395 400
Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
405 410 415
Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
420 425 430
Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
435 440 445
Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
450 455 460
Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
465 470 475 480
Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
485 490 495
Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
500 505 510
Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
515 520 525
Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
530 535 540
Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
545 550 555 560
Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
565 570 575
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
580 585 590
Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
595 600 605
Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
610 615 620

Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
625 630 635 640

Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
645 650 655

Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
660 665

<210> 106

<211> 908

<212> DNA

<213> Pasteurella multocida

<220>

<223> lgtC

<220>

<221> CDS

<222> (1)..(906)

<400> 106

atg aat att tta ttt gtt tct gat gat gtt tat gct aaa cat ctg gtg 48
Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
1 5 10 15

gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96
Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
20 25 30

tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
35 40 45

gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
50 55 60

gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240
Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
65 70 75 80

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta 288
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
85 90 95

aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta 336
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
100 105 110

gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt 384
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
115 120 125

tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att 432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
130 135 140

tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt 480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145 150 155 160

aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac	528
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp	
165 170 175	
ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata	576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile	
180 185 190	
ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt	624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe	
195 200 205	
aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga	672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly	
210 215 220	
aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt	720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val	
225 230 235 240	
att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa	768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys	
245 250 255	
cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga	816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg	
260 265 270	
ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc	864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala	
275 280 285	
ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta	908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr	
290 295 300	

<210> 107

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 107

Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val	
1 5 10 15	
Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe	
20 25 30	
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn	
35 40 45	
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn	
50 55 60	
Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu	
65 70 75 80	
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu	
85 90 95	
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu	
100 105 110	

Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
 115 120 125
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
 130 135 140
 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
 145 150 155 160
 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
 165 170 175
 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
 180 185 190
 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
 195 200 205
 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly
 210 215 220
 Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
 225 230 235 240
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
 245 250 255
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg
 260 265 270
 Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
 275 280 285
 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
 290 295 300

<210> 108
 <211> 2054
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> pnp

<220>
 <221> CDS
 <222> (1)..(2052)

<400> 108
 atg gca agt atg gat gat act act gtg ttt gtc aca gtg gtt gcc aaa 48
 Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
 1 5 10 15
 aaa gat gtg aaa gaa ggt caa gac ttc ttc cca tta act gtt aac tat 96
 Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr
 20 25 30
 caa gag cgt act tat gct gca ggc cgt att cct ggt ggc ttt ttc aaa 144
 Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys
 35 40 45
 cgt gaa ggt cgt cct tct gaa ggc gaa act tta att gct cgt tta att 192

Arg	Glu	Gly	Arg	Pro	Ser	Glu	Gly	Glu	Thr	Leu	Ile	Ala	Arg	Leu	Ile		
50						55					60						
gac	cgt	cca	att	cgt	cct	ctt	ttc	cca	gaa	ggt	ttt	tat	aac	gaa	atc	240	
Asp	Arg	Pro	Ile	Arg	Pro	Leu	Phe	Pro	Glu	Gly	Phe	Tyr	Asn	Glu	Ile	80	
65					70					75							
caa	atc	gtg	gcg	aca	gtg	gtg	tct	ggt	aat	ccg	caa	att	tgt	cca	gat	288	
Gln	Ile	Val	Ala	Thr	Val	Val	Ser	Val	Asn	Pro	Gln	Ile	Cys	Pro	Asp	95	
				85					90								
tta	gtg	gca	atg	atc	ggt	gca	tct	gcg	gca	ctt	tct	tta	tca	ggt	gtg	336	
Leu	Val	Ala	Met	Ile	Gly	Ala	Ser	Ala	Ala	Leu	Ser	Leu	Ser	Gly	Val	110	
			100					105									
cca	ttt	aat	ggc	cct	atc	ggt	gcg	gca	cgt	ggt	ggt	ttt	att	gat	gat	384	
Pro	Phe	Asn	Gly	Pro	Ile	Gly	Ala	Ala	Arg	Val	Gly	Phe	Ile	Asp	Asp		
		115					120					125					
caa	ttt	gtg	tta	aac	cca	acc	atg	aac	gag	caa	aaa	caa	agc	cgt	tta	432	
Gln	Phe	Val	Leu	Asn	Pro	Thr	Met	Asn	Glu	Gln	Lys	Gln	Ser	Arg	Leu		
	130					135					140						
gac	ttg	ggt	gtc	gcg	gga	aca	gat	aaa	gcg	gtg	tta	atg	gtg	gaa	tct	480	
Asp	Leu	Val	Val	Ala	Gly	Thr	Asp	Lys	Ala	Val	Leu	Met	Val	Glu	Ser	160	
145					150					155							
gaa	gcc	gat	gta	tta	acc	gaa	gaa	caa	atg	tta	gct	gcg	gtg	gtg	ttt	528	
Glu	Ala	Asp	Val	Leu	Thr	Glu	Glu	Gln	Met	Leu	Ala	Ala	Val	Val	Phe		
				165					170								
ggt	cat	cag	caa	caa	caa	gtg	gtg	att	gac	gcg	atc	aaa	gaa	ttt	acc	576	
Gly	His	Gln	Gln	Gln	Gln	Val	Val	Ile	Asp	Ala	Ile	Lys	Glu	Phe	Thr		
			180					185					190				
gca	gaa	gcc	ggt	aaa	ccg	cgt	tgg	gat	tgg	gtg	gca	cct	gaa	cca	aat	624	
Ala	Glu	Ala	Gly	Lys	Pro	Arg	Trp	Asp	Trp	Val	Ala	Pro	Glu	Pro	Asn		
		195					200					205					
acc	gcg	tta	att	gaa	aaa	gtg	aaa	gcg	att	gca	gaa	gcg	cgt	tta	ggc	672	
Thr	Ala	Leu	Ile	Glu	Lys	Val	Lys	Ala	Ile	Ala	Glu	Ala	Arg	Leu	Gly		
	210					215					220						
gaa	gca	tac	cgt	atc	act	gaa	aaa	caa	gca	cgt	tat	gaa	caa	att	gat	720	
Glu	Ala	Tyr	Arg	Ile	Thr	Glu	Lys	Gln	Ala	Arg	Tyr	Glu	Gln	Ile	Asp	240	
225					230					235							
gcg	att	aaa	gct	gat	gtg	att	gca	caa	atc	aca	gct	gaa	gta	gca	gaa	768	
Ala	Ile	Lys	Ala	Asp	Val	Ile	Ala	Gln	Ile	Thr	Ala	Glu	Val	Ala	Glu		
				245					250					255			
ggc	gaa	gac	atc	agt	gaa	ggg	aaa	att	gtc	gat	att	ttc	acc	gca	ctt	816	
Gly	Glu	Asp	Ile	Ser	Glu	Gly	Lys	Ile	Val	Asp	Ile	Phe	Thr	Ala	Leu		
			260				265						270				
gaa	agc	caa	atc	gta	cgt	agc	cgt	atc	att	gct	ggt	gaa	cca	cgt	att	864	
Glu	Ser	Gln	Ile	Val	Arg	Ser	Arg	Ile	Ile	Ala	Gly	Glu	Pro	Arg	Ile		
		275					280					285					
gat	ggt	cgt	aca	gtg	gat	act	gtt	cgt	gca	tta	gat	att	tgt	act	ggt	912	
Asp	Gly	Arg	Thr	Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile	Cys	Thr	Gly		
	290					295					300						

gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr 305 310 315 320	960
cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile 325 330 335	1008
att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr 340 345 350	1056
aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro 355 360 365	1104
aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala 370 375 380	1152
gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val 385 390 395 400	1200
tct gaa atc aca gaa tca aat ggt tct tct tct atg gca tcg gtt tgt Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys 405 410 415	1248
ggt gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala 420 425 430	1296
gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val 435 440 445	1344
gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp 450 455 460	1392
ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp 465 470 475 480	1440
atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn 485 490 495	1488
caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala 500 505 510	1536
atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr 515 520 525	1584
act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly 530 535 540	1632
ggt gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp 545 550 555 560	1680

545	550	555	560	
atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca				1728
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser				
	565	570	575	
gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa				1776
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu				
	580	585	590	
gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt				1824
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly				
	595	600	605	
gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct				1872
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser				
	610	615	620	
caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg				1920
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val				
	625	630	635	640
ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt				1968
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg				
	645	650	655	
att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat				2016
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp				
	660	665	670	
tct gtt gtc gca gac gtt gcc gca gaa gaa aac gca ta				2054
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala				
	675	680		

<210> 109

<211> 684

<212> PRT

<213> Pasteurella multocida

<400> 109

Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys	
1 5 10 15	
Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr	
20 25 30	
Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys	
35 40 45	
Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile	
50 55 60	
Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile	
65 70 75 80	
Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp	
85 90 95	
Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val	
100 105 110	

Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp
 115 120 125
 Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu
 130 135 140
 Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser
 145 150 155 160
 Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe
 165 170 175
 Gly His Gln Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr
 180 185 190
 Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn
 195 200 205
 Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly
 210 215 220
 Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp
 225 230 235 240
 Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu
 245 250 255
 Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu
 260 265 270
 Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile
 275 280 285
 Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly
 290 295 300
 Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr
 305 310 315 320
 Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile
 325 330 335
 Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr
 340 345 350
 Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro
 355 360 365
 Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala
 370 375 380
 Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val
 385 390 395 400
 Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys
 405 410 415
 Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala
 420 425 430
 Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val
 435 440 445

Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp
 450 455 460
 Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp
 465 470 475 480
 Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn
 485 490 495
 Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala
 500 505 510
 Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr
 515 520 525
 Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly
 530 535 540
 Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp
 545 550 555 560
 Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser
 565 570 575
 Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu
 580 585 590
 Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly
 595 600 605
 Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser
 610 615 620
 Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val
 625 630 635 640
 Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg
 645 650 655
 Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp
 660 665 670
 Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala
 675 680

<210> 110
 <211> 1514
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> purF

<220>
 <221> CDS
 <222> (1) .. (1512)

<400> 110
 atg tgt ggt att gtt ggt att gtt agc caa agc ccc gtt aac caa tca 48
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
 1 5 10 15

att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc	96
Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala	
20 25 30	
ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg	144
Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala	
35 40 45	
aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta	192
Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu	
50 55 60	
caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc	240
Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser	
65 70 75 80	
tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc	288
Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly	
85 90 95	
tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa	336
Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys	
100 105 110	
gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat	384
Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp	
115 120 125	
tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa	432
Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu	
130 135 140	
aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg	480
Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr	
145 150 155 160	
cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt	528
His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly	
165 170 175	
cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg	576
His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val	
180 185 190	
tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc	624
Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser	
195 200 205	
gaa agt atc gca tta gat aca gtg ggt ttt gag ttt gta cga gat gta	672
Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val	
210 215 220	
caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct	720
Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala	
225 230 235 240	
cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt gaa tac	768
Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr	
245 250 255	
gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat	816
Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr	
260 265 270	

gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg 275 280 285	864
gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu 290 295 300	912
acc tct aac gat att gct tta cgt att gcg cgc gtg tta aat aaa ccg Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro 305 310 315 320	960
tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile 325 330 335	1008
atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn 340 345 350	1056
acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp 355 360 365	1104
tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg 370 375 380	1152
gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile 385 390 395 400	1200
cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu 405 410 415	1248
atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val 420 425 430	1296
gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln 435 440 445	1344
caa gaa aat cca agt att caa gac ttt gat tgt tcg gtg ttt aca ggg Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly 450 455 460	1392
gtt tat gtg acg ggc gat att aca cct gaa tat ctg gat aat att gca Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala 465 470 475 480	1440
gaa cag cgt aat gat atc gcc aag aaa aag cgt gaa aaa gat gct acc Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr 485 490 495	1488
aat ctt gaa atg cac aat gaa aaa ta Asn Leu Glu Met His Asn Glu Lys 500	1514

<210> 111

<211> 504
 <212> PRT
 <213> Pasteurella multocida

<400> 111

Met	Cys	Gly	Ile	Val	Gly	Ile	Val	Ser	Gln	Ser	Pro	Val	Asn	Gln	Ser	1	5	10	15
Ile	Tyr	Asp	Ala	Leu	Thr	Leu	Leu	Gln	His	Arg	Gly	Gln	Asp	Ala	Ala	20	25	30	
Gly	Ile	Val	Thr	Val	Asp	Asp	Glu	Asn	Arg	Phe	Arg	Leu	Arg	Lys	Ala	35	40	45	
Asn	Gly	Leu	Val	Ser	Asp	Val	Phe	Glu	Gln	Val	His	Met	Leu	Arg	Leu	50	55	60	
Gln	Gly	Asn	Ala	Gly	Ile	Gly	His	Val	Arg	Tyr	Pro	Thr	Ala	Gly	Ser	65	70	75	80
Ser	Ser	Val	Ser	Glu	Ala	Gln	Pro	Phe	Tyr	Val	Asn	Ser	Pro	Tyr	Gly	85	90	95	
Leu	Thr	Leu	Val	His	Asn	Gly	Asn	Leu	Thr	Asn	Ser	Ser	Glu	Leu	Lys	100	105	110	
Glu	Lys	Leu	Phe	Arg	Leu	Ala	Arg	Arg	His	Val	Asn	Thr	Asn	Ser	Asp	115	120	125	
Ser	Glu	Leu	Leu	Leu	Asn	Ile	Leu	Ala	Asn	His	Leu	Asp	His	Phe	Glu	130	135	140	
Lys	Tyr	Gln	Leu	Asp	Pro	Gln	Asp	Val	Phe	Ser	Ala	Val	Lys	Gln	Thr	145	150	155	160
His	Gln	Asp	Ile	Arg	Gly	Ala	Tyr	Ala	Cys	Ile	Ala	Met	Ile	Ile	Gly	165	170	175	
His	Gly	Met	Val	Ala	Phe	Arg	Asp	Pro	Asn	Gly	Ile	Arg	Pro	Leu	Val	180	185	190	
Leu	Gly	Lys	Arg	Glu	Glu	Asn	Gly	Lys	Thr	Glu	Tyr	Met	Phe	Ala	Ser	195	200	205	
Glu	Ser	Ile	Ala	Leu	Asp	Thr	Val	Gly	Phe	Glu	Phe	Val	Arg	Asp	Val	210	215	220	
Gln	Pro	Gly	Glu	Ala	Ile	Tyr	Val	Thr	Phe	Glu	Gly	Glu	Met	Tyr	Ala	225	230	235	240
Gln	Gln	Cys	Ala	Asp	Lys	Pro	Thr	Leu	Thr	Pro	Cys	Ile	Phe	Glu	Tyr	245	250	255	
Val	Tyr	Phe	Ala	Arg	Pro	Asp	Ser	Cys	Ile	Asp	Gly	Val	Ser	Val	Tyr	260	265	270	
Ala	Ala	Arg	Val	His	Met	Gly	Gln	Arg	Leu	Gly	Glu	Lys	Ile	Ala	Arg	275	280	285	
Glu	Trp	Ala	Asp	Val	Asp	Asp	Ile	Asp	Val	Val	Ile	Pro	Val	Pro	Glu	290	295	300	

Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro
 305 310 315 320
 Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile
 325 330 335
 Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn
 340 345 350
 Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp
 355 360 365
 Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg
 370 375 380
 Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile
 385 390 395 400
 Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu
 405 410 415
 Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val
 420 425 430
 Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln
 435 440 445
 Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
 450 455 460
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
 465 470 475 480
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
 485 490 495
 Asn Leu Glu Met His Asn Glu Lys
 500

<210> 112
 <211> 989
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> rci

<220>
 <221> CDS
 <222> (1)..(987)

<400> 112
 atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc 48
 Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
 1 5 10 15
 aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct 96
 Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
 20 25 30
 aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa 144

Asn	Ala	Trp	Ala	Val	Asp	Glu	Glu	Arg	Lys	Leu	Ala	Asp	Leu	Ala	Lys		
		35					40					45					
ggt	atc	gct	cca	gat	att	att	ttt	aga	gat	gta	ata	gaa	cgc	tat	caa	192	
Gly	Ile	Ala	Pro	Asp	Ile	Ile	Phe	Arg	Asp	Val	Ile	Glu	Arg	Tyr	Gln		
	50					55				60							
aat	gaa	gtg	tct	ata	act	aaa	aaa	ggc	gcg	cga	aat	gaa	att	ata	aga	240	
Asn	Glu	Val	Ser	Ile	Thr	Lys	Lys	Gly	Ala	Arg	Asn	Glu	Ile	Ile	Arg		
	65				70					75					80		
tta	aac	cgc	ttt	tta	aga	tat	gat	att	tct	aat	ctg	tat	att	cgt	gat	288	
Leu	Asn	Arg	Phe	Leu	Arg	Tyr	Asp	Ile	Ser	Asn	Leu	Tyr	Ile	Arg	Asp		
				85					90					95			
tta	aga	aaa	gaa	gat	ttt	gag	gag	tgg	atc	aga	att	cgc	cta	acc	gaa	336	
Leu	Arg	Lys	Glu	Asp	Phe	Glu	Glu	Trp	Ile	Arg	Ile	Arg	Leu	Thr	Glu		
			100					105					110				
gta	tcg	gat	gct	agc	gtt	aga	cgt	gag	ctt	gtt	act	ata	tcg	tca	gtg	384	
Val	Ser	Asp	Ala	Ser	Val	Arg	Arg	Glu	Leu	Val	Thr	Ile	Ser	Ser	Val		
		115					120					125					
ctg	aca	aca	gca	ata	aat	aag	tgg	gga	tat	att	tca	agg	cat	cca	atg	432	
Leu	Thr	Thr	Ala	Ile	Asn	Lys	Trp	Gly	Tyr	Ile	Ser	Arg	His	Pro	Met		
	130					135					140						
act	ggt	att	gaa	aaa	cca	aaa	aac	tcg	gca	gaa	aga	aaa	gaa	cga	tat	480	
Thr	Gly	Ile	Glu	Lys	Pro	Lys	Asn	Ser	Ala	Glu	Arg	Lys	Glu	Arg	Tyr		
	145				150					155					160		
tca	gaa	cag	gac	att	aaa	aca	ata	tta	gaa	aca	gct	aga	tat	tgt	gaa	528	
Ser	Glu	Gln	Asp	Ile	Lys	Thr	Ile	Leu	Glu	Thr	Ala	Arg	Tyr	Cys	Glu		
				165					170					175			
gat	aaa	cta	ccc	ata	aca	ctc	aaa	caa	aga	gta	gca	att	gca	atg	tta	576	
Asp	Lys	Leu	Pro	Ile	Thr	Leu	Lys	Gln	Arg	Val	Ala	Ile	Ala	Met	Leu		
			180					185					190				
ttt	gct	att	gaa	acc	gct	atg	cgt	gct	ggt	gag	att	gct	agt	ata	aaa	624	
Phe	Ala	Ile	Glu	Thr	Ala	Met	Arg	Ala	Gly	Glu	Ile	Ala	Ser	Ile	Lys		
		195					200					205					
tgg	gat	aat	gtt	ttt	ctt	gaa	aag	aga	ata	gta	cat	tta	ccg	aca	act	672	
Trp	Asp	Asn	Val	Phe	Leu	Glu	Lys	Arg	Ile	Val	His	Leu	Pro	Thr	Thr		
	210					215					220						
aaa	aac	ggg	cac	tct	aga	gat	gtg	ccg	ctt	tcg	caa	aga	gct	gtt	gcg	720	
Lys	Asn	Gly	His	Ser	Arg	Asp	Val	Pro	Leu	Ser	Gln	Arg	Ala	Val	Ala		
	225				230					235					240		
cta	att	tta	aaa	atg	aaa	gag	gta	gaa	aat	gga	gat	ctt	gtg	ttt	cag	768	
Leu	Ile	Leu	Lys	Met	Lys	Glu	Val	Glu	Asn	Gly	Asp	Leu	Val	Phe	Gln		
				245					250					255			
acc	acg	cct	gaa	tca	tta	agc	acc	acg	ttt	aga	gtg	tta	aag	aaa	gag	816	
Thr	Thr	Pro	Glu	Ser	Leu	Ser	Thr	Thr	Phe	Arg	Val	Leu	Lys	Lys	Glu		
			260					265					270				
tgt	gga	ctt	gaa	cat	ctc	cat	ttt	cat	gat	acg	aga	agg	gaa	gcg	ttg	864	
Cys	Gly	Leu	Glu	His	Leu	His	Phe	His	Asp	Thr	Arg	Arg	Glu	Ala	Leu		
		275					280					285					

acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc 912
 Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
 290 295 300

gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat 960
 Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
 305 310 315 320

atg agt gaa gtg gca aac ttg ttg gat ta 989
 Met Ser Glu Val Ala Asn Leu Leu Asp
 325

<210> 113

<211> 329

<212> PRT

<213> Pasteurella multocida

<400> 113

Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
 1 5 10 15

Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
 20 25 30

Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys
 35 40 45

Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln
 50 55 60

Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg
 65 70 75 80

Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp
 85 90 95

Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu
 100 105 110

Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val
 115 120 125

Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met
 130 135 140

Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr
 145 150 155 160

Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu
 165 170 175

Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu
 180 185 190

Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys
 195 200 205

Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr
 210 215 220

Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala

225		230		235		240
Leu Ile Leu Lys Met	Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln					
	245		250		255	
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu						
	260		265		270	
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu						
	275		280		285	
Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser						
	290		295		300	
Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn						
305		310		315		320
Met Ser Glu Val Ala Asn Leu Leu Asp						
	325					

<210> 114
 <211> 1190
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> sopE
 <220>
 <221> CDS
 <222> (1)..(1188)

<400> 114	
atg tct gaa gaa tat cta cat ggt gtc aaa gtc aca gaa atc aat caa	48
Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln	
1 5 10 15	
gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc	96
Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val	
20 25 30	
tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc	144
Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro	
35 40 45	
gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa	192
Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln	
50 55 60	
ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc	240
Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys	
65 70 75 80	
aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa	288
Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu	
85 90 95	
aca aaa gca agt gaa atg aac acg gca att att ggc aca atc aca gaa	336
Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu	
100 105 110	

gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa	384
Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys	
115 120 125	
ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa	432
Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys	
130 135 140	
gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt	480
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe	
145 150 155 160	
gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa	528
Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln	
165 170 175	
tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat	576
Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp	
180 185 190	
ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc	624
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala	
195 200 205	
gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc	672
Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly	
210 215 220	
tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gtc	720
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val	
225 230 235 240	
aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac	768
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn	
245 250 255	
tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt	816
Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe	
260 265 270	
cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt	864
Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe	
275 280 285	
gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg	912
Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly	
290 295 300	
gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa	960
Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys	
305 310 315 320	
gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa	1008
Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys	
325 330 335	
ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt	1056
Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser	
340 345 350	
gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac	1104
Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His	

355	360	365	
cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat			1152
Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp			
370	375	380	
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Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser			
385	390	395	
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Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro			
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Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln			
	50	55	60
Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys			
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Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu			
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Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu			
	100	105	110
Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys			
	115	120	125
Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys			
	130	135	140
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe			
	145	150	155
Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln			
	165	170	175
Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp			
	180	185	190
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala			
	195	200	205
Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly			
	210	215	220
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val			
	225	230	235
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn			

				245					250					255					
Tyr	Leu	Asn	Glu	Gln	Gly	Ile	Thr	Cys	Cys	Val	Asn	His	Asn	Gly	Phe				
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Arg	Phe	Trp	Gly	Leu	Arg	Thr	Thr	Ala	Glu	Asp	Pro	Leu	Phe	Lys	Phe				
		275					280					285							
Glu	Val	Tyr	Thr	Arg	Thr	Ala	Gln	Ile	Leu	Lys	Asp	Thr	Ile	Ala	Gly				
	290					295					300								
Ala	Phe	Asp	Trp	Ala	Val	Asp	Lys	Asp	Ile	Ser	Val	Thr	Leu	Val	Lys				
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Asp	Ile	Ile	Glu	Ala	Ile	Asn	Ala	Lys	Trp	Arg	Asp	Tyr	Thr	Thr	Lys				
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Gly	Tyr	Leu	Ile	Gly	Gly	Lys	Ala	Trp	Leu	Asn	Lys	Glu	Leu	Asn	Ser				
			340					345					350						
Ala	Thr	Asn	Leu	Lys	Asp	Ala	Lys	Leu	Leu	Ile	Ser	Tyr	Asp	Tyr	His				
		355					360					365							
Pro	Val	Pro	Pro	Leu	Glu	Gln	Leu	Gly	Phe	Asn	Gln	Tyr	Ile	Ser	Asp				
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Glu	Tyr	Leu	Val	Asp	Phe	Ser	Asn	Arg	Leu	Ala	Ser								
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1				5				10						15		
ctt	gta	cct	gtt	gct	gaa	acg	att	aat	tct	gca	gta	gga	aat	gcc	tca	96
Leu	Val	Pro	Val	Ala	Glu	Thr	Ile	Asn	Ser	Ala	Val	Gly	Asn	Ala	Ser	
		20						25						30		
tca	aaa	gac	gtt	tct	gac	acc	gag	ata	agt	gct	tct	caa	cca	gcg	ctc	144
Ser	Lys	Asp	Val	Ser	Asp	Thr	Glu	Ile	Ser	Ala	Ser	Gln	Pro	Ala	Leu	
		35				40						45				
aac	tcg	ccg	ctt	tcg	acc	ctt	tct	gta	tta	gtc	aaa	acc	gca	ttt	aat	192
Asn	Ser	Pro	Leu	Ser	Thr	Leu	Ser	Val	Leu	Val	Lys	Thr	Ala	Phe	Asn	
50						55						60				
ccg	gtt	tca	aca	ttg	atg	tcg	ttg	act	tgg	aaa	gaa	tac	gcc	gtt	tta	240

Pro	Val	Ser	Thr	Leu	Met	Ser	Leu	Thr	Trp	Lys	Glu	Tyr	Ala	Val	Leu		
65					70					75					80		
tta	tta	agt	gtg	gtg	tct	ttt	cct	ctt	atg	gca	caa	gcc	tct	gat	aca	288	
Leu	Leu	Ser	Val	Val	Ser	Phe	Pro	Leu	Met	Ala	Gln	Ala	Ser	Asp	Thr		
				85					90					95			
gat	tca	gtg	gta	caa	aga	aaa	cct	gaa	tta	act	gat	gtg	acg	aat	agc	336	
Asp	Ser	Val	Val	Gln	Arg	Lys	Pro	Glu	Leu	Thr	Asp	Val	Thr	Asn	Ser		
			100					105					110				
aac	agc	tat	cat	gtg	gaa	tta	gat	aga	gag	cat	cat	aaa	ggg	gag	cat	384	
Asn	Ser	Tyr	His	Val	Glu	Leu	Asp	Arg	Glu	His	His	Lys	Gly	Glu	His		
		115					120					125					
caa	aca	aaa	atc	aaa	cat	act	gag	aat	aat	gtc	atc	att	gtt	gat	att	432	
Gln	Thr	Lys	Ile	Lys	His	Thr	Glu	Asn	Asn	Val	Ile	Ile	Val	Asp	Ile		
	130					135					140						
gca	aaa	cca	aac	caa	aag	ggc	att	tca	gat	aac	cgt	ttt	aaa	cac	ttc	480	
Ala	Lys	Pro	Asn	Gln	Lys	Gly	Ile	Ser	Asp	Asn	Arg	Phe	Lys	His	Phe		
145					150					155					160		
aac	atc	cca	aat	ggg	gcg	gta	ttt	aac	aat	agc	gcc	aag	gaa	aaa	cgc	528	
Asn	Ile	Pro	Asn	Gly	Ala	Val	Phe	Asn	Asn	Ser	Ala	Lys	Glu	Lys	Arg		
				165				170						175			
tca	cag	tta	gtg	ggg	tat	ttg	cca	ggt	aac	cag	aat	tta	acg	gaa	ggt	576	
Ser	Gln	Leu	Val	Gly	Tyr	Leu	Pro	Gly	Asn	Gln	Asn	Leu	Thr	Glu	Gly		
			180					185					190				
agt	gaa	gca	aaa	gcg	atc	tta	aat	cag	gtg	act	gga	ccg	gat	gcc	agt	624	
Ser	Glu	Ala	Lys	Ala	Ile	Leu	Asn	Gln	Val	Thr	Gly	Pro	Asp	Ala	Ser		
		195					200					205					
aaa	att	gaa	ggc	gcc	ctt	gaa	att	tta	ggg	caa	aaa	gcc	gat	ttg	gtg	672	
Lys	Ile	Glu	Gly	Ala	Leu	Glu	Ile	Leu	Gly	Gln	Lys	Ala	Asp	Leu	Val		
	210					215					220						
att	gcg	aac	caa	aat	ggc	att	gtg	ctt	aat	ggg	gta	aaa	acc	att	aat	720	
Ile	Ala	Asn	Gln	Asn	Gly	Ile	Val	Leu	Asn	Gly	Val	Lys	Thr	Ile	Asn		
225					230					235					240		
gcc	aat	cgt	ttt	gtg	gca	aca	acc	agt	agt	acc	att	gat	cct	gag	caa	768	
Ala	Asn	Arg	Phe	Val	Ala	Thr	Thr	Ser	Ser	Thr	Ile	Asp	Pro	Glu	Gln		
				245					250					255			
atg	cag	tta	aat	gtc	acg	caa	ggt	aca	gtg	aca	att	ggg	gtg	gat	gga	816	
Met	Gln	Leu	Asn	Val	Thr	Gln	Gly	Thr	Val	Thr	Ile	Gly	Val	Asp	Gly		
			260					265					270				
ttt	gcc	aca	gat	ggc	tta	cct	tat	ttg	gat	atc	att	gcc	aaa	aag	att	864	
Phe	Ala	Thr	Asp	Gly	Leu	Pro	Tyr	Leu	Asp	Ile	Ile	Ala	Lys	Lys	Ile		
		275					280					285					
gaa	caa	aaa	caa	gcg	att	aca	aaa	gaa	aga	aca	gga	aat	tcc	gaa	acc	912	
Glu	Gln	Lys	Gln	Ala	Ile	Thr	Lys	Glu	Arg	Thr	Gly	Asn	Ser	Glu	Thr		
	290					295					300						
gat	atc	act	ttt	gtc	gca	ggt	aac	agt	aaa	tat	gat	tta	aag	aca	cat	960	
Asp	Ile	Thr	Phe	Val	Ala	Gly	Asn	Ser	Lys	Tyr	Asp	Leu	Lys	Thr	His		
305					310					315					320		

caa gtg aca gaa aag cat acc gct gag gca caa ggt gaa att gcg att	1008
Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile	
325 330 335	
agc ggt gcg agt acc ggt gca atg tac ggt aaa aat atc aaa tta atc	1056
Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile	
340 345 350	
gta acg gat aaa ggc gct ggg gta aaa cat gat ggc att att tta tct	1104
Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser	
355 360 365	
gag gcg gat att caa att gaa acc cat gag ggc gat gtt gaa tta ggc	1152
Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly	
370 375 380	
aat aca aaa aat aat cag aat gag aat tat gcc aaa gct cat gcg gaa	1200
Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu	
385 390 395 400	
ggg aat ttt acg gtt aaa ggc ggt aag cac gtt att att ggt aag gaa	1248
Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu	
405 410 415	
gtt aaa gcc aac aaa gcg gtc gat att caa gca caa gaa aca aca gta	1296
Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val	
420 425 430	
aga caa aat gcg aaa tta act gcc aaa acg agt gcc aaa att aca gca	1344
Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala	
435 440 445	
agt aag agt gtg aat ctt gaa gat aac gcg aaa ctt att gct aat gag	1392
Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu	
450 455 460	
ctg agc aca aca acc aat aaa tta acc aat aaa ggt agc att tac ggc	1440
Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly	
465 470 475 480	
aag aaa gtg acg cta gat gct gat aat tta gtc aat agt aaa gaa atc	1488
Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile	
485 490 495	
tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta	1536
Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu	
500 505 510	
ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca	1584
Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser	
515 520 525	
ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt	1632
Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly	
530 535 540	
aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga	1680
Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly	
545 550 555 560	
aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat	1728
Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn	

565										570					575					
ggt	caa	att	gat	caa	gcg	aaa	aat	att	caa	tta	aac	gcg	aat	atc	acg	1776				
Val	Gln	Ile	Asp	Gln	Ala	Lys	Asn	Ile	Gln	Leu	Asn	Ala	Asn	Ile	Thr					
			580					585					590							
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Ile	Asn	Thr	Lys	Ser	Gly	Phe	Val	Asn	Tyr	Gly	Thr	Leu	Ala	Ser	Ala					
		595					600					605								
caa	aat	tta	acg	att	aat	acc	gaa	caa	ggc	agc	att	tat	aac	ata	ggc	1872				
Gln	Asn	Leu	Thr	Ile	Asn	Thr	Glu	Gln	Gly	Ser	Ile	Tyr	Asn	Ile	Gly					
	610					615					620									
ggt	atc	ttg	ggg	gcg	ggt	aaa	agt	ttg	aat	ctg	agc	gcg	aaa	aga	gga	1920				
Gly	Ile	Leu	Gly	Ala	Gly	Lys	Ser	Leu	Asn	Leu	Ser	Ala	Lys	Arg	Gly					
625					630					635					640					
gaa	aac	caa	gga	gga	tat	ctt	att	aat	caa	ggt	aag	agt	cta	ctc	cat	1968				
Glu	Asn	Gln	Gly	Gly	Tyr	Leu	Ile	Asn	Gln	Gly	Lys	Ser	Leu	Leu	His					
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tct	gaa	ggc	gcc	atg	aac	ctc	aca	gcg	gat	cgc	acg	gtg	tac	aat	tta	2016				
Ser	Glu	Gly	Ala	Met	Asn	Leu	Thr	Ala	Asp	Arg	Thr	Val	Tyr	Asn	Leu					
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ggg	aat	att	ttt	gct	aaa	ggt	gac	gcg	acg	atc	aat	gca	aac	gcg	tta	2064				
Gly	Asn	Ile	Phe	Ala	Lys	Gly	Asp	Ala	Thr	Ile	Asn	Ala	Asn	Ala	Leu					
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att	aat	gat	ggt	act	ctc	aca	ggt	cgt	ctt	gag	tat	caa	gat	ctg	aaa	2112				
Ile	Asn	Asp	Val	Thr	Leu	Thr	Gly	Arg	Leu	Glu	Tyr	Gln	Asp	Leu	Lys					
		690				695					700									
aaa	gat	tat	acg	cgt	tat	tat	cgt	atc	aat	gaa	acg	gca	aaa	cat	ggt	2160				
Lys	Asp	Tyr	Thr	Arg	Tyr	Tyr	Arg	Ile	Asn	Glu	Thr	Ala	Lys	His	Gly					
705					710					715					720					
tgg	cat	aat	aac	ttc	tat	gaa	tta	aac	gtc	gac	aga	ggt	tct	tg		2204				
Trp	His	Asn	Asn	Phe	Tyr	Glu	Leu	Asn	Val	Asp	Arg	Val	Ser							
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<210> 117

<211> 734

<212> PRT

<213> Pasteurella multocida

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Ser	Lys	Asp	Val	Ser	Asp	Thr	Glu	Ile	Ser	Ala	Ser	Gln	Pro	Ala	Leu
		35				40						45			

Asn	Ser	Pro	Leu	Ser	Thr	Leu	Ser	Val	Leu	Val	Lys	Thr	Ala	Phe	Asn
	50					55					60				

Pro	Val	Ser	Thr	Leu	Met	Ser	Leu	Thr	Trp	Lys	Glu	Tyr	Ala	Val	Leu
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65	70	75	80
Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr	85	90	95
Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser	100	105	110
Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His	115	120	125
Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile	130	135	140
Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe	145	150	155
Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg	165	170	175
Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly	180	185	190
Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser	195	200	205
Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val	210	215	220
Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn	225	230	235
Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln	245	250	255
Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly	260	265	270
Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile	275	280	285
Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr	290	295	300
Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His	305	310	315
Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile	325	330	335
Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile	340	345	350
Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser	355	360	365
Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly	370	375	380
Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu	385	390	395
Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu			

405					410					415					
Val	Lys	Ala	Asn	Lys	Ala	Val	Asp	Ile	Gln	Ala	Gln	Glu	Thr	Thr	Val
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Arg	Gln	Asn	Ala	Lys	Leu	Thr	Ala	Lys	Thr	Ser	Ala	Lys	Ile	Thr	Ala
		435					440					445			
Ser	Lys	Ser	Val	Asn	Leu	Glu	Asp	Asn	Ala	Lys	Leu	Ile	Ala	Asn	Glu
	450					455					460				
Leu	Ser	Thr	Thr	Thr	Asn	Lys	Leu	Thr	Asn	Lys	Gly	Ser	Ile	Tyr	Gly
465					470					475					480
Lys	Lys	Val	Thr	Leu	Asp	Ala	Asp	Asn	Leu	Val	Asn	Ser	Lys	Glu	Ile
				485					490					495	
Tyr	Ala	Ser	Ser	Glu	Leu	Asp	Ile	Gln	Thr	Lys	Gly	Arg	Asp	Leu	Leu
			500					505					510		
Leu	Glu	Asp	Gly	Val	Asn	Gln	Pro	Leu	Ser	Phe	Leu	Lys	Gly	Ala	Ser
		515					520					525			
Leu	Leu	Ala	Pro	Gly	Phe	Val	Asn	Thr	Gly	Leu	Ile	His	Ser	Asn	Gly
	530					535					540				
Asn	Ala	Lys	Leu	Thr	Phe	Lys	Asp	Asp	Thr	Ser	Phe	Val	Thr	Glu	Gly
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Asn	Asn	Phe	Ile	Thr	Ala	Lys	Asp	Asn	Leu	Glu	Ile	Thr	Ala	Lys	Asn
				565					570					575	
Val	Gln	Ile	Asp	Gln	Ala	Lys	Asn	Ile	Gln	Leu	Asn	Ala	Asn	Ile	Thr
			580					585					590		
Ile	Asn	Thr	Lys	Ser	Gly	Phe	Val	Asn	Tyr	Gly	Thr	Leu	Ala	Ser	Ala
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Gln	Asn	Leu	Thr	Ile	Asn	Thr	Glu	Gln	Gly	Ser	Ile	Tyr	Asn	Ile	Gly
	610					615					620				
Gly	Ile	Leu	Gly	Ala	Gly	Lys	Ser	Leu	Asn	Leu	Ser	Ala	Lys	Arg	Gly
625					630					635					640
Glu	Asn	Gln	Gly	Gly	Tyr	Leu	Ile	Asn	Gln	Gly	Lys	Ser	Leu	Leu	His
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Ser	Glu	Gly	Ala	Met	Asn	Leu	Thr	Ala	Asp	Arg	Thr	Val	Tyr	Asn	Leu
			660					665					670		
Gly	Asn	Ile	Phe	Ala	Lys	Gly	Asp	Ala	Thr	Ile	Asn	Ala	Asn	Ala	Leu
		675					680					685			
Ile	Asn	Asp	Val	Thr	Leu	Thr	Gly	Arg	Leu	Glu	Tyr	Gln	Asp	Leu	Lys
	690					695					700				
Lys	Asp	Tyr	Thr	Arg	Tyr	Tyr	Arg	Ile	Asn	Glu	Thr	Ala	Lys	His	Gly
705					710					715					720
Trp	His	Asn	Asn	Phe	Tyr	Glu	Leu	Asn	Val	Asp	Arg	Val	Ser		
				725					730						

<210> 118
 <211> 251
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unkO

<220>
 <221> CDS
 <222> (1)..(249)

<400> 118
 atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1 5 10 15
 gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
 20 25 30
 tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
 35 40 45
 gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192
 Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
 50 55 60
 agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
 65 70 75 80
 tgt aat cat ta 251
 Cys Asn His

<210> 119
 <211> 83
 <212> PRT
 <213> Pasteurella multocida

<400> 119
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1 5 10 15
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
 20 25 30
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
 35 40 45
 Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
 50 55 60
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
 65 70 75 80
 Cys Asn His

<210> 120

<211> 548
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unkP

<220>
 <221> CDS
 <222> (1)..(546)

<400> 120

atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att tca	48
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser	
1 5 10 15	
aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat ttt	96
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe	
20 25 30	
gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa ggc	144
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly	
35 40 45	
atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta cgc	192
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg	
50 55 60	
acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act	240
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr	
65 70 75 80	
gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca gtg	288
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val	
85 90 95	
gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc	336
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile	
100 105 110	
aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc ggt	384
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly	
115 120 125	
aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat	432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp	
130 135 140	
gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa	480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu	
145 150 155 160	
cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt	528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe	
165 170 175	
tca aat cgt tta gca tcg ta	548
Ser Asn Arg Leu Ala Ser	
180	

<210> 121
 <211> 182

<212> PRT

<213> Pasteurella multocida

<400> 121

Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1 5 10 15
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
20 25 30
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
35 40 45
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175
Ser Asn Arg Leu Ala Ser
180

<210> 122

<211> 69

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvA-or1

<220>

<221> CDS

<222> (1) .. (69)

<400> 122

atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
1 5 10 15
gat aag ttt aag ata ctt agc 69
Asp Lys Phe Lys Ile Leu Ser
20

<210> 123
 <211> 23
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 123
 Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
 1 5 10 15

Asp Lys Phe Lys Ile Leu Ser
 20

<210> 124
 <211> 64
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvA-or2

<220>
 <221> CDS
 <222> (3)..(62)

<400> 124
 ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta 47
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu
 1 5 10 15

ttg gca agc atg aca ta 64
 Leu Ala Ser Met Thr
 20

<210> 125
 <211> 20
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 125
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu
 1 5 10 15

Ala Ser Met Thr
 20

<210> 126
 <211> 653
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvB

<220>
 <221> CDS
 <222> (1)..(651)

<400> 126
 tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc 48
 Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala

1	5	10	15	
gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa	96			
Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys				
20 25 30				
cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt	144			
His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly				
35 40 45				
aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa	192			
Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu				
50 55 60				
caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt	240			
Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe				
65 70 75 80				
gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt	288			
Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser				
85 90 95				
att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat	336			
Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr				
100 105 110				
aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa	384			
Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu				
115 120 125				
gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa	432			
Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys				
130 135 140				
tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca	480			
Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser				
145 150 155 160				
agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa	528			
Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln				
165 170 175				
tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct	576			
Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala				
180 185 190				
tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat	624			
Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn				
195 200 205				
ctt ggc atg ggt tta tct gtc ggt tgg at	653			
Leu Gly Met Gly Leu Ser Val Gly Trp				
210 215				

<210> 127

<211> 217

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 127

Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1 5 10 15
 Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
 20 25 30
 His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
 35 40 45
 Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
 50 55 60
 Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
 65 70 75 80
 Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
 85 90 95
 Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
 100 105 110
 Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
 115 120 125
 Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
 130 135 140
 Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
 145 150 155 160
 Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
 165 170 175
 Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
 180 185 190
 Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
 195 200 205
 Leu Gly Met Gly Leu Ser Val Gly Trp
 210 215

<210> 128

<211> 242

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvC

<220>

<221> CDS

<222> (1)..(240)

<400> 128

atg tgg cgg atg gga gat ttt atg tct aaa aaa gag agg ctg aat gat 48
 Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1 5 10 15
 atg gct cgc cag att tta tca gcg gcg gag ttg ctc att gca aag gaa 96
 Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
 20 25 30


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ggt ttg caa aat tta tct atg agg aaa atc gca agt gaa gcc ggt atc 144
Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
      35                40                45

gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg 192
Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
      50                55                60

gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat 240
Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
      65                70                75                80

at 242

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<210> 129
<211> 80
<212> PRT
<213> Actinobacillus pleuropneumoniae

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<400> 129
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
  1                5                10                15

Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
      20                25                30

Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
      35                40                45

Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
      50                55                60

Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
      65                70                75                80

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<210> 130
<211> 527
<212> DNA
<213> Actinobacillus pleuropneumoniae

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<220>
<223> apvD

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<220>
<221> CDS
<222> (1)..(525)

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<400> 130
aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa 48
Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
  1                5                10                15

caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96
Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
      20                25                30

gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144
Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
      35                40                45

gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192

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Asp	Pro	Arg	Leu	Ala	Glu	Thr	Glu	Leu	Lys	Leu	Ala	Lys	Ala	Glu	Leu		
50						55					60						
gca	aat	gct	tct	gct	aat	ttg	gat	aca	aaa	aaa	att	aat	ctt	aag	caa	240	
Ala	Asn	Ala	Ser	Ala	Asn	Leu	Asp	Thr	Lys	Lys	Ile	Asn	Leu	Lys	Gln		
65					70					75					80		
ctg	caa	tca	gat	tgg	gaa	cgt	cat	caa	cgt	ttg	ata	cga	acc	aat	gcg	288	
Leu	Gln	Ser	Asp	Trp	Glu	Arg	His	Gln	Arg	Leu	Ile	Arg	Thr	Asn	Ala		
				85					90					95			
aca	agc	caa	aag	gaa	aca	gaa	gaa	gca	aaa	agt	aga	tta	aat	acg	gcc	336	
Thr	Ser	Gln	Lys	Glu	Thr	Glu	Glu	Ala	Lys	Ser	Arg	Leu	Asn	Thr	Ala		
			100					105					110				
aaa	gca	gaa	ctt	caa	att	gcg	caa	aat	aat	cta	gat	atc	gct	aaa	atc	384	
Lys	Ala	Glu	Leu	Gln	Ile	Ala	Gln	Asn	Asn	Leu	Asp	Ile	Ala	Lys	Ile		
		115					120					125					
aga	gtg	gaa	aaa	gct	gaa	acc	gaa	cta	gga	tat	aca	gaa	att	cgt	tct	432	
Arg	Val	Glu	Lys	Ala	Glu	Thr	Glu	Leu	Gly	Tyr	Thr	Glu	Ile	Arg	Ser		
	130					135					140						
cca	ctt	gat	gca	aca	gta	att	tca	gta	ttt	gcg	caa	aat	ggt	caa	act	480	
Pro	Leu	Asp	Ala	Thr	Val	Ile	Ser	Val	Phe	Ala	Gln	Asn	Gly	Gln	Thr		
145					150				155					160			
tta	gtc	acc	acc	caa	caa	gta	cca	gtg	ctg	atg	aaa	tta	gct	aat	at	527	
Leu	Val	Thr	Thr	Gln	Gln	Val	Pro	Val	Leu	Met	Lys	Leu	Ala	Asn			
				165					170					175			

<210> 131

<211> 175

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 131

Asn	Ile	Gln	Lys	Thr	Val	Ile	Ala	Ser	Gly	Thr	Leu	Gln	Ala	Thr	Glu		
1				5					10					15			
Gln	Val	Asp	Ile	Gly	Ala	Gln	Val	Ser	Gly	Gln	Ile	Lys	His	Ile	Leu		
		20						25					30				
Val	Gln	Glu	Gly	Gln	Lys	Val	Lys	Lys	Gly	Glu	Leu	Leu	Ala	Val	Ile		
		35					40					45					
Asp	Pro	Arg	Leu	Ala	Glu	Thr	Glu	Leu	Lys	Leu	Ala	Lys	Ala	Glu	Leu		
50						55					60						
Ala	Asn	Ala	Ser	Ala	Asn	Leu	Asp	Thr	Lys	Lys	Ile	Asn	Leu	Lys	Gln		
65					70					75					80		
Leu	Gln	Ser	Asp	Trp	Glu	Arg	His	Gln	Arg	Leu	Ile	Arg	Thr	Asn	Ala		
			85						90					95			
Thr	Ser	Gln	Lys	Glu	Thr	Glu	Glu	Ala	Lys	Ser	Arg	Leu	Asn	Thr	Ala		
			100					105					110				
Lys	Ala	Glu	Leu	Gln	Ile	Ala	Gln	Asn	Asn	Leu	Asp	Ile	Ala	Lys	Ile		
		115					120					125					
Arg	Val	Glu	Lys	Ala	Glu	Thr	Glu	Leu	Gly	Tyr	Thr	Glu	Ile	Arg	Ser		

130	135	140	
Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr			
145	150	155	160
Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn			
	165	170	175
<210> 132			
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<212> DNA			
<213> Actinobacillus pleuropneumoniae			
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<223> atpG			
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<221> CDS			
<222> (1) .. (864)			
<400> 132			
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Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn			
1	5	10	15
act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg			96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met			
	20	25	30
cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca			144
Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr			
	35	40	45
atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag			192
Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys			
	50	55	60
cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc			240
His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val			
	65	70	75
gtt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc			288
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe			
	85	90	95
aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt			336
Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser			
	100	105	110
gtt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat			384
Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn			
	115	120	125
cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg			432
Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro			
	130	135	140
gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc			480
Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe			
145	150	155	160
cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa			528

Arg	Asn	Gly	Glu	Val	Asp	Ala	Val	Tyr	Val	Ala	Tyr	Asn	Arg	Phe	Glu	
				165					170					175		
aat	acg	atg	tca	caa	aaa	cct	gtt	atc	gca	cag	tta	ctt	ccg	tta	cct	576
Asn	Thr	Met	Ser	Gln	Lys	Pro	Val	Ile	Ala	Gln	Leu	Leu	Pro	Leu	Pro	
			180					185					190			
aaa	cta	gat	gac	gat	gaa	tta	gat	acg	aaa	ggg	tca	tgg	gat	tat	att	624
Lys	Leu	Asp	Asp	Asp	Glu	Leu	Asp	Thr	Lys	Gly	Ser	Trp	Asp	Tyr	Ile	
		195					200					205				
tat	gaa	ccg	aat	cca	caa	gtt	tta	ttg	gat	agt	tta	ctt	gtt	cgt	tat	672
Tyr	Glu	Pro	Asn	Pro	Gln	Val	Leu	Leu	Asp	Ser	Leu	Leu	Val	Arg	Tyr	
	210					215					220					
tta	gaa	act	cag	gta	tac	caa	gca	gtt	gta	gat	aac	cta	gct	tct	gaa	720
Leu	Glu	Thr	Gln	Val	Tyr	Gln	Ala	Val	Val	Asp	Asn	Leu	Ala	Ser	Glu	
	225				230					235					240	
caa	gcc	gct	cga	atg	gta	gcg	atg	aaa	gcc	gca	aca	gat	aat	gcg	ggg	768
Gln	Ala	Ala	Arg	Met	Val	Ala	Met	Lys	Ala	Ala	Thr	Asp	Asn	Ala	Gly	
			245					250						255		
aca	tta	atc	gat	gaa	tta	caa	tta	gtg	tat	aac	aaa	gct	cgc	caa	gca	816
Thr	Leu	Ile	Asp	Glu	Leu	Gln	Leu	Val	Tyr	Asn	Lys	Ala	Arg	Gln	Ala	
			260					265					270			
agc	att	aca	aat	gaa	tta	aac	gaa	att	gtt	gcg	ggg	gcc	gca	gca	att	864
Ser	Ile	Thr	Asn	Glu	Leu	Asn	Glu	Ile	Val	Ala	Gly	Ala	Ala	Ala	Ile	
		275					280					285				
taa																867

<210> 133

<211> 288

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 133

Met	Ala	Gly	Ala	Lys	Glu	Ile	Arg	Thr	Lys	Ile	Ala	Ser	Val	Lys	Asn
1				5					10					15	

Thr	Gln	Lys	Ile	Thr	Lys	Ala	Met	Glu	Met	Val	Ala	Thr	Ser	Lys	Met
			20					25					30		

Arg	Lys	Thr	Gln	Glu	Arg	Met	Ala	Ala	Ser	Arg	Pro	Tyr	Ser	Glu	Thr
		35					40					45			

Ile	Arg	Lys	Val	Ile	Ser	His	Ile	Ala	Lys	Gly	Ser	Ile	Gly	Tyr	Lys
	50					55					60				

His	Pro	Phe	Leu	Thr	Glu	Arg	Asp	Ile	Lys	Lys	Val	Gly	Tyr	Leu	Val
	65				70					75					80

Val	Ser	Thr	Asp	Arg	Gly	Leu	Cys	Gly	Gly	Leu	Asn	Ile	Asn	Leu	Phe
				85					90					95	

Lys	Ala	Thr	Leu	Asn	Glu	Phe	Lys	Thr	Trp	Lys	Asp	Lys	Asp	Val	Ser
			100					105					110		

Val	Glu	Leu	Gly	Leu	Val	Gly	Ser	Lys	Gly	Val	Ser	Phe	Tyr	Gln	Asn
		115					120					125			

Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro
 130 135 140
 Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe
 145 150 155 160
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu
 165 170 175
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro
 180 185 190
 Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile
 195 200 205
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr
 210 215 220
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
 225 230 235 240
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
 245 250 255
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
 260 265 270
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
 275 280 285

<210> 134
 <211> 534
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> atpH

<220>
 <221> CDS
 <222> (1)..(531)

<400> 134
 atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt 48
 Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1 5 10 15
 gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta 96
 Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
 20 25 30
 cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att 144
 Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
 35 40 45
 aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc 192
 Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
 50 55 60
 tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg 240
 Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met

65	70	75	80	
gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc				288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe				
	85	90	95	
gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt				336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val				
	100	105	110	
tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg				384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala				
	115	120	125	
atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat				432
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp				
	130	135	140	
aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att				480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile				
	145	150	155	160
gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc				528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser				
	165	170	175	
ttg taa				534
Leu				
<210> 135				
<211> 177				
<212> PRT				
<213> Actinobacillus pleuropneumoniae				
<400> 135				
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe				
1	5	10	15	
Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu				
	20	25	30	
Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile				
	35	40	45	
Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile				
	50	55	60	
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met				
	65	70	75	80
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe				
	85	90	95	
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val				
	100	105	110	
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala				
	115	120	125	
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp				
	130	135	140	

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
 145 150 155 160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
 165 170 175

Leu

<210> 136

<211> 321

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> dksA

<220>

<221> CDS

<222> (1)..(318)

<400> 136

gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa 48
 Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1 5 10 15

atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act 96
 Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
 20 25 30

cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt 144
 Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
 35 40 45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac 192
 Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
 50 55 60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt 240
 Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
 65 70 75 80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt 288
 Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
 85 90 95

gcg gaa atc cgt gaa aag caa atg ggc tta taa 321
 Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
 100 105

<210> 137

<211> 106

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 137

Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1 5 10 15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
 20 25 30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
35 40 45

Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
50 55 60

Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
65 70 75 80

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
85 90 95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
100 105

<210> 138
<211> 33
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> dnaK

<220>
<221> CDS
<222> (1)..(30)

<400> 138
gct gag ttt gaa gaa gtg aaa gat aat aaa taa
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
1 5 10

33

<210> 139
<211> 10
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 139
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
1 5 10

<210> 140
<211> 453
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> exbB

<220>
<221> CDS
<222> (1)..(450)

<400> 140
atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
1 5 10 15 48

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att
Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
96

20										25										30										
gaa	cgc	gta	ctt	ttc	tac	aaa	caa	ttg	gat	gtg	acc	aaa	tat	gac	acg	144														
Glu	Arg	Val	Leu	Phe	Tyr	Lys	Gln	Leu	Asp	Val	Thr	Lys	Tyr	Asp	Thr															
35			40				45																							
cta	caa	gat	ttg	gaa	att	gat	acc	act	cgc	aat	tta	acc	acc	att	tcc	192														
Leu	Gln	Asp	Leu	Glu	Ile	Asp	Thr	Thr	Arg	Asn	Leu	Thr	Thr	Ile	Ser															
50			55				60																							
act	atc	ggg	gcc	aac	gcc	cct	tat	atc	ggg	tta	tta	gga	acc	gta	tta	240														
Thr	Ile	Gly	Ala	Asn	Ala	Pro	Tyr	Ile	Gly	Leu	Leu	Gly	Thr	Val	Leu															
65			70				75				80																			
ggg	atc	tta	ctt	acc	ttc	tat	cat	tta	ggg	cat	tcc	ggc	ggg	gat	att	288														
Gly	Ile	Leu	Leu	Thr	Phe	Tyr	His	Leu	Gly	His	Ser	Gly	Gly	Asp	Ile															
85				90				95																						
gac	gcc	gca	tcc	att	atg	gtt	cac	ctt	tgc	ctt	gca	tta	aaa	gca	acc	336														
Asp	Ala	Ala	Ser	Ile	Met	Val	His	Leu	Ser	Leu	Ala	Leu	Lys	Ala	Thr															
100			105				110																							
gca	gcc	ggg	atc	tta	gtc	gct	att	ccg	gca	atg	atg	ttc	tac	agc	ggg	384														
Ala	Ala	Gly	Ile	Leu	Val	Ala	Ile	Pro	Ala	Met	Met	Phe	Tyr	Ser	Gly															
115			120				125																							
ttt	aac	cgt	aaa	gtg	gat	gaa	agc	aaa	ctt	aaa	tgg	caa	gcg	att	caa	432														
Phe	Asn	Arg	Lys	Val	Asp	Glu	Ser	Lys	Leu	Lys	Trp	Gln	Ala	Ile	Gln															
130			135				140																							
gct	cgt	aaa	gcc	aat	caa	taa										453														
Ala	Arg	Lys	Ala	Asn	Gln																									
145			150																											

<210> 141

<211> 150

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 141

Met	Glu	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	His	Val	Asp	Tyr	Ile	Ile
1				5					10					15	

Leu	Gly	Leu	Leu	Leu	Leu	Met	Ser	Val	Val	Leu	Val	Trp	Lys	Ile	Ile
		20					25						30		

Glu	Arg	Val	Leu	Phe	Tyr	Lys	Gln	Leu	Asp	Val	Thr	Lys	Tyr	Asp	Thr
		35					40					45			

Leu	Gln	Asp	Leu	Glu	Ile	Asp	Thr	Thr	Arg	Asn	Leu	Thr	Thr	Ile	Ser
	50					55					60				

Thr	Ile	Gly	Ala	Asn	Ala	Pro	Tyr	Ile	Gly	Leu	Leu	Gly	Thr	Val	Leu
65					70					75					80

Gly	Ile	Leu	Leu	Thr	Phe	Tyr	His	Leu	Gly	His	Ser	Gly	Gly	Asp	Ile
				85					90					95	

Asp	Ala	Ala	Ser	Ile	Met	Val	His	Leu	Ser	Leu	Ala	Leu	Lys	Ala	Thr
			100					105					110		

Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
 115 120 125

Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
 130 135 140

Ala Arg Lys Ala Asn Gln
 145 150

<210> 142

<211> 720

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> fkpA

<220>

<221> CDS

<222> (1)..(717)

<400> 142

atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc 48
 Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
 1 5 10 15

gtt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat 96
 Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
 20 25 30

tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc 144
 Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
 35 40 45

gtt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg 192
 Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
 50 55 60

gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa 240
 Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
 65 70 75 80

gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa 288
 Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
 85 90 95

gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt 336
 Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
 100 105 110

aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc 384
 Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
 115 120 125

gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg 432
 Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
 130 135 140

cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc 480
 Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
 145 150 155 160

gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa	528
Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu	
165 170 175	
ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg	576
Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met	
180 185 190	
ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt	624
Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly	
195 200 205	
tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa	672
Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys	
210 215 220	
ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa	720
Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys	
225 230 235	

<210> 143

<211> 239

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 143

Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe	
1 5 10 15	
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp	
20 25 30	
Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val	
35 40 45	
Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu	
50 55 60	
Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu	
65 70 75 80	
Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln	
85 90 95	
Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly	
100 105 110	
Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr	
115 120 125	
Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser	
130 135 140	
Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr	
145 150 155 160	
Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu	
165 170 175	
Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met	
180 185 190	

Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
195 200 205

Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
210 215 220

Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
225 230 235

<210> 144

<211> 290

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> HI0379

<220>

<221> CDS

<222> (3)..(287)

<400> 144

tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa 47
His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln
1 5 10 15

cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95
Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn
20 25 30

ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct 143
Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser
35 40 45

cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt 191
Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly
50 55 60

gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg 239
Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser
65 70 75

gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat 287
Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
80 85 90 95

taa 290

<210> 145

<211> 95

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 145

His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln Pro
1 5 10 15

Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn Leu
20 25 30

Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser Gln

35 40 45

Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val
50 55 60

Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp
65 70 75 80

His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
85 90 95

<210> 146
<211> 273
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> hupA

<220>
<221> CDS
<222> (1) .. (270)

<400> 146
atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta 48
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu
1 5 10 15

agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc 96
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile
20 25 30

tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt 144
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly
35 40 45

act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt 192
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg
50 55 60

acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt 240
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val
65 70 75 80

gca ggt aaa gca tta aaa gat tta gta aaa taa 273
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys
85 90

<210> 147
<211> 90
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 147
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu
1 5 10 15

Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile
20 25 30

Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly
35 40 45
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg
50 55 60
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val
65 70 75 80
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys
85 90

<210> 148
<211> 551
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> lpdA

<220>
<221> CDS
<222> (1) .. (549)

<400> 148
atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct 48
Met Ser Lys Glu Ile Lys Thr Gln Val Val Leu Gly Ala Gly Pro
1 5 10 15
gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca 96
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
20 25 30
gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta 144
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
35 40 45
ggc tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa 192
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
50 55 60
gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac 240
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
65 70 75 80
att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa 288
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
85 90 95
tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta 336
Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
100 105 110
gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt 384
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
115 120 125
gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432
Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
130 135 140
gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480

Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
 145 150 155 160
 ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
 165 170 175
 gaa aaa att act cat tat ggg cc 551
 Glu Lys Ile Thr His Tyr Gly
 180

<210> 149
 <211> 183
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 149
 Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro
 1 5 10 15
 Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
 20 25 30
 Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
 35 40 45
 Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
 50 55 60
 Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
 65 70 75 80
 Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
 85 90 95
 Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
 100 105 110
 Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
 115 120 125
 Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
 130 135 140
 Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
 145 150 155 160
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
 165 170 175
 Glu Lys Ile Thr His Tyr Gly
 180

<210> 150
 <211> 1095
 <212> DNA
 <213> Actinobacillus pleuropneumoniae
 <220>
 <223> Omp5-2

<220>

<221> CDS

<222> (1)..(1092)

<400> 150

atg	aaa	aaa	tca	tta	gtt	gct	tta	aca	gta	tta	tcg	gct	gca	gcg	gta	48
Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Thr	Val	Leu	Ser	Ala	Ala	Ala	Val	
1				5					10					15		
gct	caa	gca	gcg	cca	caa	caa	aat	act	ttc	tac	gca	ggt	gcg	aaa	gca	96
Ala	Gln	Ala	Ala	Pro	Gln	Gln	Asn	Thr	Phe	Tyr	Ala	Gly	Ala	Lys	Ala	
			20					25					30			
ggt	tgg	gcg	tca	ttc	cat	gat	ggt	atc	gaa	caa	tta	gat	tca	gct	aaa	144
Gly	Trp	Ala	Ser	Phe	His	Asp	Gly	Ile	Glu	Gln	Leu	Asp	Ser	Ala	Lys	
		35					40					45				
aac	aca	gat	cgc	ggt	aca	aaa	tac	ggt	atc	aac	cgt	aat	tca	gta	act	192
Asn	Thr	Asp	Arg	Gly	Thr	Lys	Tyr	Gly	Ile	Asn	Arg	Asn	Ser	Val	Thr	
	50					55					60					
tac	ggc	gta	ttc	ggc	ggt	tac	caa	att	tta	aac	caa	gac	aaa	tta	ggt	240
Tyr	Gly	Val	Phe	Gly	Gly	Tyr	Gln	Ile	Leu	Asn	Gln	Asp	Lys	Leu	Gly	
65				70					75					80		
tta	gcg	gct	gaa	tta	ggt	tat	gac	tat	ttc	ggt	cgt	gtg	cgc	ggt	tct	288
Leu	Ala	Ala	Glu	Leu	Gly	Tyr	Asp	Tyr	Phe	Gly	Arg	Val	Arg	Gly	Ser	
			85						90					95		
gaa	aaa	cca	aac	ggt	aaa	gcg	gac	aag	aaa	act	ttc	cgt	cac	gct	gca	336
Glu	Lys	Pro	Asn	Gly	Lys	Ala	Asp	Lys	Lys	Thr	Phe	Arg	His	Ala	Ala	
		100						105					110			
cac	ggt	gcg	aca	atc	gca	tta	aaa	cct	agc	tac	gaa	gta	tta	cct	gac	384
His	Gly	Ala	Thr	Ile	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp	
		115					120					125				
tta	gac	gtt	tac	ggt	aaa	gta	ggt	atc	gca	tta	gta	aac	aat	aca	tat	432
Leu	Asp	Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Leu	Val	Asn	Asn	Thr	Tyr	
	130					135					140					
aaa	aca	ttc	aat	gca	gca	caa	gag	aaa	gtg	aaa	act	cgt	cgt	ttc	caa	480
Lys	Thr	Phe	Asn	Ala	Ala	Gln	Glu	Lys	Val	Lys	Thr	Arg	Arg	Phe	Gln	
145					150				155					160		
agt	tct	tta	att	tta	ggt	gcg	ggt	gtt	gag	tac	gca	att	ctt	cct	gaa	528
Ser	Ser	Leu	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro	Glu	
				165				170					175			
tta	gcg	gca	cgt	gtt	gaa	tac	caa	tgg	tta	aac	aac	gca	ggt	aaa	gca	576
Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Trp	Leu	Asn	Asn	Ala	Gly	Lys	Ala	
			180					185					190			
agc	tac	tct	act	tta	aat	cgt	atg	ggt	gca	act	gac	tac	cgt	tcg	gat	624
Ser	Tyr	Ser	Thr	Leu	Asn	Arg	Met	Gly	Ala	Thr	Asp	Tyr	Arg	Ser	Asp	
		195					200					205				
atc	agt	tcc	gta	tct	gca	ggt	tta	agc	tac	cgt	ttc	ggt	caa	ggt	gcg	672
Ile	Ser	Ser	Val	Ser	Ala	Gly	Leu	Ser	Tyr	Arg	Phe	Gly	Gln	Gly	Ala	
	210					215					220					
gca	ccg	gtt	gca	gct	ccg	gca	gtt	gaa	act	aaa	aac	ttc	gca	ttc	agc	720

Ala	Pro	Val	Ala	Ala	Pro	Ala	Val	Glu	Thr	Lys	Asn	Phe	Ala	Phe	Ser		
225					230					235					240		
tct	gac	gta	tta	ttc	gca	ttc	ggg	aaa	tca	aac	tta	aaa	ccg	gct	gcg	768	
Ser	Asp	Val	Leu	Phe	Ala	Phe	Gly	Lys	Ser	Asn	Leu	Lys	Pro	Ala	Ala		
				245				250					255				
gca	aca	gca	tta	gat	gca	atg	caa	acc	gaa	atc	aat	aac	gca	ggg	tta	816	
Ala	Thr	Ala	Leu	Asp	Ala	Met	Gln	Thr	Glu	Ile	Asn	Asn	Ala	Gly	Leu		
			260					265					270				
tca	aat	gct	gcg	atc	caa	gta	aac	ggg	tac	acg	gac	cgt	atc	ggg	aaa	864	
Ser	Asn	Ala	Ala	Ile	Gln	Val	Asn	Gly	Tyr	Thr	Asp	Arg	Ile	Gly	Lys		
		275					280					285					
gaa	gct	tca	aac	tta	aaa	ctt	tca	caa	cgt	cgt	gcg	gaa	aca	gta	gct	912	
Glu	Ala	Ser	Asn	Leu	Lys	Leu	Ser	Gln	Arg	Arg	Ala	Glu	Thr	Val	Ala		
	290					295					300						
aac	tac	atc	gtt	tct	aaa	ggg	gct	ccg	gca	gct	aac	gta	act	gca	gta	960	
Asn	Tyr	Ile	Val	Ser	Lys	Gly	Ala	Pro	Ala	Ala	Asn	Val	Thr	Ala	Val		
305					310				315						320		
ggg	tac	ggg	gaa	gca	aac	cct	gta	acc	ggc	gca	aca	tgt	gac	aaa	gtt	1008	
Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala	Thr	Cys	Asp	Lys	Val		
				325					330					335			
aaa	ggg	cgt	aaa	gca	tta	atc	gct	tgc	tta	gca	ccg	gat	cgt	cgt	gtt	1056	
Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala	Pro	Asp	Arg	Arg	Val		
			340					345					350				
gaa	gtt	caa	gtt	caa	ggg	act	aaa	gaa	gta	act	atg	taa				1095	
Glu	Val	Gln	Val	Gln	Gly	Thr	Lys	Glu	Val	Thr	Met						
		355					360										

<210> 151

<211> 364

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 151

Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Thr	Val	Leu	Ser	Ala	Ala	Ala	Val
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Ala	Gln	Ala	Ala	Pro	Gln	Gln	Asn	Thr	Phe	Tyr	Ala	Gly	Ala	Lys	Ala
		20						25					30		

Gly	Trp	Ala	Ser	Phe	His	Asp	Gly	Ile	Glu	Gln	Leu	Asp	Ser	Ala	Lys
	35						40					45			

Asn	Thr	Asp	Arg	Gly	Thr	Lys	Tyr	Gly	Ile	Asn	Arg	Asn	Ser	Val	Thr
	50					55					60				

Tyr	Gly	Val	Phe	Gly	Gly	Tyr	Gln	Ile	Leu	Asn	Gln	Asp	Lys	Leu	Gly
65					70					75					80

Leu	Ala	Ala	Glu	Leu	Gly	Tyr	Asp	Tyr	Phe	Gly	Arg	Val	Arg	Gly	Ser
				85					90					95	

Glu	Lys	Pro	Asn	Gly	Lys	Ala	Asp	Lys	Lys	Thr	Phe	Arg	His	Ala	Ala
			100					105					110		

His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp
 115 120 125
 Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr
 130 135 140
 Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln
 145 150 155 160
 Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu
 165 170 175
 Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala
 180 185 190
 Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp
 195 200 205
 Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala
 210 215 220
 Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser
 225 230 235 240
 Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala
 245 250 255
 Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu
 260 265 270
 Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys
 275 280 285
 Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala
 290 295 300
 Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
 305 310 315 320
 Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
 325 330 335
 Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val
 340 345 350
 Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
 355 360

<210> 152
 <211> 1110
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> Omp5

<220>
 <221> CDS
 <222> (1) .. (1107)

<400> 152

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Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Ala	Val	Leu	Ser	Ala	Ala	Ala	Val	
1				5					10					15		
gct	caa	gca	gct	cca	caa	caa	aat	act	ttc	tac	gca	ggg	gca	aaa	gtt	96
Ala	Gln	Ala	Ala	Pro	Gln	Gln	Asn	Thr	Phe	Tyr	Ala	Gly	Ala	Lys	Val	
			20					25					30			
ggg	caa	tca	tca	ttt	cac	cac	ggg	gtt	aac	caa	tta	aaa	tct	ggg	cac	144
Gly	Gln	Ser	Ser	Phe	His	His	Gly	Val	Asn	Gln	Leu	Lys	Ser	Gly	His	
		35					40					45				
gat	gat	cgt	tat	aat	gat	aaa	aca	cgt	aag	tat	ggg	atc	aac	cgt	aac	192
Asp	Asp	Arg	Tyr	Asn	Asp	Lys	Thr	Arg	Lys	Tyr	Gly	Ile	Asn	Arg	Asn	
	50					55					60					
tct	gta	act	tac	ggg	gta	ttc	ggc	ggg	tac	caa	atc	tta	aac	caa	aat	240
Ser	Val	Thr	Tyr	Gly	Val	Phe	Gly	Gly	Tyr	Gln	Ile	Leu	Asn	Gln	Asn	
65					70				75						80	
aac	ttc	ggg	tta	gca	gct	gaa	tta	ggc	tat	gac	tac	tac	ggg	cgc	gta	288
Asn	Phe	Gly	Leu	Ala	Ala	Glu	Leu	Gly	Tyr	Asp	Tyr	Tyr	Gly	Arg	Val	
				85					90					95		
cgt	ggg	aac	gta	gat	gaa	ttc	cgt	aca	gtt	aaa	cac	tct	gct	cac	ggg	336
Arg	Gly	Asn	Val	Asp	Glu	Phe	Arg	Thr	Val	Lys	His	Ser	Ala	His	Gly	
			100					105					110			
tta	aac	tta	gca	tta	aaa	cca	agc	tac	gaa	gta	tta	cct	gac	tta	gac	384
Leu	Asn	Leu	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp	Leu	Asp	
		115					120					125				
gtt	tac	ggg	aaa	gta	ggg	att	gca	gtt	gtt	cgt	aat	gac	tat	aaa	aaa	432
Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Val	Val	Arg	Asn	Asp	Tyr	Lys	Lys	
	130					135					140					
tat	ggg	gca	gaa	aac	act	aac	gaa	tca	aca	aca	aaa	ttc	cac	aaa	tta	480
Tyr	Gly	Ala	Glu	Asn	Thr	Asn	Glu	Ser	Thr	Thr	Lys	Phe	His	Lys	Leu	
145					150				155						160	
aaa	gca	tca	act	att	tta	ggg	gca	ggg	gtt	gag	tac	gca	att	cct	cct	528
Lys	Ala	Ser	Thr	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro	
				165					170					175		
gaa	tta	gca	gca	cgt	gtt	gaa	tac	caa	tac	tta	aac	aaa	gca	ggg	aac	576
Glu	Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Tyr	Leu	Asn	Lys	Ala	Gly	Asn	
			180					185					190			
tta	aat	aaa	gca	tta	gtt	cgt	tca	ggc	aca	caa	gat	gtg	gac	ttc	caa	624
Leu	Asn	Lys	Ala	Leu	Val	Arg	Ser	Gly	Thr	Gln	Asp	Val	Asp	Phe	Gln	
		195					200					205				
tat	gct	cct	gat	atc	cac	tct	gta	aca	gca	ggg	tta	tca	tac	cgt	ttc	672
Tyr	Ala	Pro	Asp	Ile	His	Ser	Val	Thr	Ala	Gly	Leu	Ser	Tyr	Arg	Phe	
	210					215					220					
ggg	caa	ggc	gct	gta	gca	cca	gtt	gtt	gag	cca	gaa	gtt	gta	act	aaa	720
Gly	Gln	Gly	Ala	Val	Ala	Pro	Val	Val	Glu	Pro	Glu	Val	Val	Thr	Lys	
225					230				235						240	
aac	ttc	gca	ttc	agc	tca	gac	gtt	tta	ttt	gat	ttc	ggg	aaa	tca	agc	768
Asn	Phe	Ala	Phe	Ser	Ser	Asp	Val	Leu	Phe	Asp	Phe	Gly	Lys	Ser	Ser	

245								250				255				
tta	aaa	cca	gca	gca	gca	aca	gct	tta	gac	gca	gct	aac	act	gaa	atc	816
Leu	Lys	Pro	Ala	Ala	Ala	Thr	Ala	Leu	Asp	Ala	Ala	Asn	Thr	Glu	Ile	
			260											270		
gct	aac	tta	ggg	tta	gca	act	cca	gct	atc	caa	gtt	aac	ggg	tat	aca	864
Ala	Asn	Leu	Gly	Leu	Ala	Thr	Pro	Ala	Ile	Gln	Val	Asn	Gly	Tyr	Thr	
		275					280					285				
gac	cgt	atc	ggg	aaa	gaa	gct	tca	aac	tta	aaa	ctt	tca	caa	cgc	cgt	912
Asp	Arg	Ile	Gly	Lys	Glu	Ala	Ser	Asn	Leu	Lys	Leu	Ser	Gln	Arg	Arg	
	290					295					300					
gca	gaa	act	gta	gct	aac	tac	tta	gtt	tct	aaa	ggg	caa	aac	cct	gca	960
Ala	Glu	Thr	Val	Ala	Asn	Tyr	Leu	Val	Ser	Lys	Gly	Gln	Asn	Pro	Ala	
305					310					315				320		
aac	gta	act	gca	gta	ggg	tac	ggg	gaa	gca	aac	cca	gta	acc	ggc	gca	1008
Asn	Val	Thr	Ala	Val	Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala	
			325						330					335		
aca	tgt	gat	gca	gtt	aaa	ggg	cgt	aaa	gca	tta	atc	gct	tgc	tta	gca	1056
Thr	Cys	Asp	Ala	Val	Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala	
			340				345						350			
ccg	gat	cgt	cgt	gtt	gaa	gtt	caa	gta	caa	ggg	gct	aaa	aac	gta	gct	1104
Pro	Asp	Arg	Arg	Val	Glu	Val	Gln	Val	Gln	Gly	Ala	Lys	Asn	Val	Ala	
		355				360						365				
atg	taa															1110
Met																

<210> 153

<211> 369

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 153

Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Ala	Val	Leu	Ser	Ala	Ala	Ala	Val
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Ala	Gln	Ala	Ala	Pro	Gln	Gln	Asn	Thr	Phe	Tyr	Ala	Gly	Ala	Lys	Val
		20						25					30		
Gly	Gln	Ser	Ser	Phe	His	His	Gly	Val	Asn	Gln	Leu	Lys	Ser	Gly	His
		35					40					45			
Asp	Asp	Arg	Tyr	Asn	Asp	Lys	Thr	Arg	Lys	Tyr	Gly	Ile	Asn	Arg	Asn
	50					55					60				
Ser	Val	Thr	Tyr	Gly	Val	Phe	Gly	Gly	Tyr	Gln	Ile	Leu	Asn	Gln	Asn
	65				70				75					80	
Asn	Phe	Gly	Leu	Ala	Ala	Glu	Leu	Gly	Tyr	Asp	Tyr	Tyr	Gly	Arg	Val
			85					90					95		
Arg	Gly	Asn	Val	Asp	Glu	Phe	Arg	Thr	Val	Lys	His	Ser	Ala	His	Gly
		100						105					110		
Leu	Asn	Leu	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp	Leu	Asp
	115						120					125			

Asn	Ile	Lys	Glu	Phe	Val	Lys	Glu	Ala	Gly	Lys	Pro	Arg	Trp	Asp	Trp		
1				5					10					15			
ggt	gag	ccg	gaa	ccg	aat	acc	gca	tta	atc	aac	caa	ggt	aaa	gag	tta	96	
Val	Ala	Pro	Glu	Pro	Asn	Thr	Ala	Leu	Ile	Asn	Gln	Val	Lys	Ala	Leu		
			20					25					30				
gag	gaa	gag	cgt	atc	ggc	gat	gag	tat	cgt	att	aca	gaa	aaa	caa	gag	144	
Ala	Glu	Ala	Arg	Ile	Gly	Asp	Ala	Tyr	Arg	Ile	Thr	Glu	Lys	Gln	Ala		
			35				40					45					
cgt	tac	gaa	caa	atc	gat	gca	att	aaa	gag	gat	ggt	atc	gca	caa	tta	192	
Arg	Tyr	Glu	Gln	Ile	Asp	Ala	Ile	Lys	Ala	Asp	Val	Ile	Ala	Gln	Leu		
	50					55					60						
acc	gca	caa	gac	gaa	acc	ggt	tct	gaa	ggc	gag	att	att	gat	att	att	240	
Thr	Ala	Gln	Asp	Glu	Thr	Val	Ser	Glu	Gly	Ala	Ile	Ile	Asp	Ile	Ile		
	65				70				75						80		
acc	gca	tta	gaa	agt	tct	att	ggt	cgc	ggc	cgt	att	att	gcc	ggc	gaa	288	
Thr	Ala	Leu	Glu	Ser	Ser	Ile	Val	Arg	Gly	Arg	Ile	Ile	Ala	Gly	Glu		
				85				90						95			
ccg	cgt	att	gac	ggc	cgt	acg	gta	gat	acg	ggt	cgt	gca	tta	gac	att	336	
Pro	Arg	Ile	Asp	Gly	Arg	Thr	Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile		
			100					105					110				
tgc	acc	ggc	gta	tta	cct	cgt	acg	cac	ggc	tct	gca	atc	ttt	act	cgc	384	
Cys	Thr	Gly	Val	Leu	Pro	Arg	Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg		
		115				120					125						
ggc	gaa	aca	caa	gca	tta	gag	ggt	gca	acc	tta	ggc	act	gag	cgc	gat	432	
Gly	Glu	Thr	Gln	Ala	Leu	Ala	Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp		
	130				135					140							
gca	caa	att	ggt	gac	gaa	tta	acc	ggc	gag	aaa	tca	gac	cgt	ttc	tta	480	
Ala	Gln	Ile	Val	Asp	Glu	Leu	Thr	Gly	Glu	Lys	Ser	Asp	Arg	Phe	Leu		
	145				150			155							160		
ttc	cac	tat	aac	ttc	cct	ccg	tac	tct	gtc	ggc	gaa	acc	ggc	cgt	atc	528	
Phe	His	Tyr	Asn	Phe	Pro	Pro	Tyr	Ser	Val	Gly	Glu	Thr	Gly	Arg	Ile		
			165					170					175				
ggc	tcg	ccg	aaa	cgt	cgt	gaa	atc	ggc	cac	ggc	cgt	tta	gag	aaa	cgc	576	
Gly	Ser	Pro	Lys	Arg	Arg	Glu	Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg		
			180					185				190					
ggc	gta	tta	gag	gta	atg	ccg	act	gct	gaa	gaa	ttc	ccg	tat	gta	gtg	624	
Gly	Val	Leu	Ala	Val	Met	Pro	Thr	Ala	Glu	Glu	Phe	Pro	Tyr	Val	Val		
		195				200						205					
cgc	gta	gta	tct	gaa	att	acc	gaa	tca	aac	ggc	tct	tct	tca	atg	gct	672	
Arg	Val	Val	Ser	Glu	Ile	Thr	Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala		
	210					215					220						
tcc	gta	tgc	ggc	gca	tct	tta	gag	tta	atg	gac	gca	ggc	gta	ccg	att	720	
Ser	Val	Cys	Gly	Ala	Ser	Leu	Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile		
	225				230					235					240		
aaa	gag	gag	ggt	gag	ggc	atc	gca	atg	ggc	tta	gtg	aaa	gaa	gaa	gaa	768	
Lys	Ala	Ala	Val	Ala	Gly	Ile	Ala	Met	Gly	Leu	Val	Lys	Glu	Glu	Glu		
				245					250					255			

aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc	816
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly	
260 265 270	
gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt	864
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu	
275 280 285	
caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc	912
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile	
290 295 300	
gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg	960
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met	
305 310 315 320	
gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct	1008
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro	
325 330 335	
cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc	1056
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile	
340 345 350	
ggt aaa ggc ggt gcg gtt at	1076
Gly Lys Gly Gly Ala Val	
355	

<210> 155
 <211> 358
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 155
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
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Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
20 25 30
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
35 40 45
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
50 55 60
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
65 70 75 80
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
85 90 95
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
100 105 110
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
115 120 125
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
130 135 140

Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
145 150 155 160

Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
165 170 175

Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
180 185 190

Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
195 200 205

Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
210 215 220

Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
225 230 235 240

Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu
245 250 255

Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly
260 265 270

Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu
275 280 285

Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile
290 295 300

Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met
305 310 315 320

Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro
325 330 335

Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile
340 345 350

Gly Lys Gly Gly Ala Val
355

<210> 156
<211> 1055
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> potD

<220>
<221> CDS
<222> (1)..(1053)

<400> 156
atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca 48
Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
1 5 10 15

tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct 96
Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala
20 25 30

caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat	144
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr	
35 40 45	
gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa	192
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys	
50 55 60	
gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta	240
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu	
65 70 75 80	
aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac	288
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn	
85 90 95	
tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat	336
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp	
100 105 110	
cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac	384
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn	
115 120 125	
aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt	432
Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly	
130 135 140	
gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc	480
Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe	
145 150 155 160	
act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa	528
Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln	
165 170 175	
tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta	576
Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu	
180 185 190	
ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac	624
Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr	
195 200 205	
gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac	672
Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp	
210 215 220	
aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta	720
Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu	
225 230 235 240	
tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gcg ccg gta aac	768
Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn	
245 250 255	
atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc	816
Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala	
260 265 270	
att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac	864
Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn	
275 280 285	

tac	tta	tta	agc	gca	ccg	gtt	gcg	gaa	aaa	tta	acg	tta	gaa	atc	ggc	912
Tyr	Leu	Leu	Ser	Ala	Pro	Val	Ala	Glu	Lys	Leu	Thr	Leu	Glu	Ile	Gly	
	290					295					300					
tat	ccg	act	tca	aac	gta	gaa	gcg	tta	aaa	aca	tta	cca	aaa	gag	att	960
Tyr	Pro	Thr	Ser	Asn	Val	Glu	Ala	Leu	Lys	Thr	Leu	Pro	Lys	Glu	Ile	
305					310					315					320	
acc	gaa	gat	ccg	gca	atc	tat	ccg	aca	gct	gat	gtg	tta	aaa	gcg	gca	1008
Thr	Glu	Asp	Pro	Ala	Ile	Tyr	Pro	Thr	Ala	Asp	Val	Leu	Lys	Ala	Ala	
				325					330					335		
caa	tg	caa	gac	gat	gta	ggc	aat	gca	atc	gaa	ctt	tac	gaa	aaa	ta	1055
Gln	Trp	Gln	Asp	Asp	Val	Gly	Asn	Ala	Ile	Glu	Leu	Tyr	Glu	Lys		
			340					345					350			

<210> 157

<211> 351

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 157

Met	Lys	Lys	Leu	Ala	Gly	Leu	Phe	Ala	Ala	Gly	Leu	Ala	Thr	Val	Ala	
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Leu	Thr	Ala	Cys	Asn	Glu	Glu	Lys	Pro	Lys	Ala	Ala	Glu	Ala	Ala	Ala	
			20					25					30			
Gln	Pro	Ala	Ala	Ala	Gly	Thr	Val	His	Leu	Tyr	Thr	Trp	Thr	Glu	Tyr	
		35					40					45				
Val	Pro	Glu	Gly	Leu	Leu	Asp	Glu	Phe	Thr	Lys	Gln	Thr	Gly	Ile	Lys	
	50					55					60					
Val	Glu	Val	Ser	Ser	Leu	Glu	Ser	Asn	Glu	Thr	Met	Tyr	Ala	Lys	Leu	
65					70					75					80	
Lys	Leu	Gln	Gly	Lys	Asp	Gly	Gly	Tyr	Asp	Val	Ile	Ala	Pro	Ser	Asn	
				85					90					95		
Tyr	Phe	Val	Ser	Lys	Met	Ala	Lys	Glu	Gly	Met	Leu	Ala	Glu	Leu	Asp	
			100					105					110			
His	Ala	Lys	Leu	Pro	Val	Ile	Lys	Glu	Leu	Asn	Gln	Asp	Trp	Leu	Asn	
		115					120					125				
Lys	Pro	Tyr	Asp	Gln	Gly	Asn	Lys	Tyr	Ser	Leu	Pro	Gln	Leu	Leu	Gly	
	130					135					140					
Ala	Pro	Gly	Ile	Ala	Phe	Asn	Ser	Asn	Asp	Tyr	Lys	Gly	Asp	Ala	Phe	
145					150					155					160	
Thr	Ser	Trp	Gly	Asp	Leu	Trp	Lys	Pro	Glu	Phe	Ala	Asn	Lys	Val	Gln	
			165						170					175		
Leu	Leu	Asp	Asp	Ala	Arg	Glu	Val	Phe	Asn	Ile	Ala	Leu	Leu	Lys	Leu	
		180						185					190			
Gly	Lys	Asn	Pro	Asn	Thr	Thr	Asn	Pro	Glu	Glu	Ile	Lys	Ala	Ala	Tyr	
		195					200					205				
Glu	Glu	Leu	Arg	Lys	Leu	Arg	Pro	Asn	Val	Leu	Ser	Phe	Thr	Ser	Asp	

210	215	220
Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu 225 230 235 240		
Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn 245 250 255		
Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala 260 265 270		
Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn 275 280 285		
Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly 290 295 300		
Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile 305 310 315 320		
Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala 325 330 335		
Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys 340 345 350		

<210> 158
 <211> 525
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> rpmF

<220>
 <221> CDS
 <222> (1)..(522)

<400> 158 atg caa aag gta aaa cta ccc ctc acc att gac cca tat aaa gac gct Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala 1 5 10 15	48
cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn 20 25 30	96
cgt ttg ggt gaa tct gtg agc aat gtg cta agc gat gca caa gtt act Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr 35 40 45	144
ctc tcg tta tat atc gat ccg caa cgc tta acc gtt att aaa ggt acg Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr 50 55 60	192
gcg aca gtg gaa gtg gaa ttc gat tgc caa cga tgc ggt aac ccg ttt Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe 65 70 75 80	240
aca caa acg ctt gac tgt tcg ttt tgt ttc agt ccg gtg tcc aat atg Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met	288

85										90					95					
gat	cag	gcg	gac	aat	ttg	ccc	gaa	att	tat	gaa	cca	atc	gaa	gta	aac	336				
Asp	Gln	Ala	Asp	Asn	Leu	Pro	Glu	Ile	Tyr	Glu	Pro	Ile	Glu	Val	Asn					
			100					105					110							
gag	ttc	ggt	gaa	gta	aat	tta	cta	gat	atg	atc	gaa	gat	gga	ttt	atc	384				
Glu	Phe	Gly	Glu	Val	Asn	Leu	Leu	Asp	Met	Ile	Glu	Asp	Gly	Phe	Ile					
		115					120					125								
atc	gaa	ttg	cct	cta	gtc	ccg	atg	cat	agt	gaa	gaa	cac	tgt	gaa	gtg	432				
Ile	Glu	Leu	Pro	Leu	Val	Pro	Met	His	Ser	Glu	Glu	His	Cys	Glu	Val					
		130				135					140									
tcc	gtg	agt	gaa	cag	gtg	ttt	ggc	gaa	ttg	cct	gaa	gaa	ttg	gcg	aaa	480				
Ser	Val	Ser	Glu	Gln	Val	Phe	Gly	Glu	Leu	Pro	Glu	Glu	Leu	Ala	Lys					
145					150					155					160					
aaa	cct	aac	ccg	ttc	gct	gta	tta	gct	aat	tta	aag	aaa	aac	tag		525				
Lys	Pro	Asn	Pro	Phe	Ala	Val	Leu	Ala	Asn	Leu	Lys	Lys	Asn							
				165					170											
<210> 159																				
<211> 174																				
<212> PRT																				
<213> Actinobacillus pleuropneumoniae																				
<400> 159																				
Met	Gln	Lys	Val	Lys	Leu	Pro	Leu	Thr	Ile	Asp	Pro	Tyr	Lys	Asp	Ala					
1				5					10					15						
Gln	Arg	Arg	Met	Asp	Tyr	Glu	Gly	Tyr	Ile	Ser	Arg	Ser	Leu	Leu	Asn					
			20					25					30							
Arg	Leu	Gly	Glu	Ser	Val	Ser	Asn	Val	Leu	Ser	Asp	Ala	Gln	Val	Thr					
		35					40					45								
Leu	Ser	Leu	Tyr	Ile	Asp	Pro	Gln	Arg	Leu	Thr	Val	Ile	Lys	Gly	Thr					
	50					55					60									
Ala	Thr	Val	Glu	Val	Glu	Phe	Asp	Cys	Gln	Arg	Cys	Gly	Asn	Pro	Phe					
65					70				75						80					
Thr	Gln	Thr	Leu	Asp	Cys	Ser	Phe	Cys	Phe	Ser	Pro	Val	Ser	Asn	Met					
				85					90					95						
Asp	Gln	Ala	Asp	Asn	Leu	Pro	Glu	Ile	Tyr	Glu	Pro	Ile	Glu	Val	Asn					
			100					105					110							
Glu	Phe	Gly	Glu	Val	Asn	Leu	Leu	Asp	Met	Ile	Glu	Asp	Gly	Phe	Ile					
		115					120					125								
Ile	Glu	Leu	Pro	Leu	Val	Pro	Met	His	Ser	Glu	Glu	His	Cys	Glu	Val					
	130					135					140									
Ser	Val	Ser	Glu	Gln	Val	Phe	Gly	Glu	Leu	Pro	Glu	Glu	Leu	Ala	Lys					
145					150					155					160					
Lys	Pro	Asn	Pro	Phe	Ala	Val	Leu	Ala	Asn	Leu	Lys	Lys	Asn							
				165					170											

<210> 160
 <211> 1302
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> tig

<220>
 <221> CDS
 <222> (1) .. (1299)

<400> 160
 atg tca att tct att gaa act tta gaa ggc tta caa cgc cgc gta act 48
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 1 5 10 15
 att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta 96
 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
 20 25 30
 aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144
 Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
 35 40 45
 gta ccg cac gca att atc gaa caa cgt ttc ggt tta gcg gct cgc caa 192
 Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
 50 55 60
 gac gta tta tcc gat gaa atg caa cgt gcg ttc ttt gat gcg gta atc 240
 Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
 65 70 75 80
 gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca ccg aac aac 288
 Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
 85 90 95
 tac caa ccg agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc 336
 Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
 100 105 110
 ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa ccg 384
 Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
 115 120 125
 gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta 432
 Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
 130 135 140
 cgt aaa caa caa gcg act tgg gct gaa tct caa gca gcg gca caa gcg 480
 Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
 145 150 155 160
 gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag 528
 Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
 165 170 175
 ttt gaa ggc ggt aaa gcg aca gac ttc act tta gca atg ggt caa agt 576
 Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
 180 185 190
 cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc gcc 624
 Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly

195	200	205	
gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu 210 215 220			672
aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val 225 230 235 240			720
gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe 245 250 255			768
ggt tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn 260 265 270			816
atg caa cgt gaa ctt aaa aac gca gta acc gca cgc gtt aaa aac caa Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln 275 280 285			864
gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala 290 295 300			912
gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg 305 310 315 320			960
ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe 325 330 335			1008
gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr 340 345 350			1056
gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu 355 360 365			1104
acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val 370 375 380			1152
gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val 385 390 395 400			1200
gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta Val Leu Glu Glu Gln Ala Val Glu Val Leu Ala Lys Ala Lys Val 405 410 415			1248
act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln 420 425 430			1296
ggc taa Gly			1302

<210> 161
 <211> 433
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 161

Met	Ser	Ile	Ser	Ile	Glu	Thr	Leu	Glu	Gly	Leu	Gln	Arg	Arg	Val	Thr
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Ile	Thr	Val	Ala	Ala	Asp	Lys	Ile	Glu	Ala	Ala	Tyr	Lys	Glu	Gln	Leu
		20						25					30		
Lys	Gly	Tyr	Ala	Lys	Asn	Ala	Arg	Val	Asp	Gly	Phe	Arg	Lys	Gly	Lys
	35						40					45			
Val	Pro	His	Ala	Ile	Ile	Glu	Gln	Arg	Phe	Gly	Leu	Ala	Ala	Arg	Gln
	50					55					60				
Asp	Val	Leu	Ser	Asp	Glu	Met	Gln	Arg	Ala	Phe	Phe	Asp	Ala	Val	Ile
65					70					75					80
Ala	Glu	Lys	Ile	Asn	Leu	Ala	Gly	Arg	Pro	Thr	Phe	Thr	Pro	Asn	Asn
				85					90					95	
Tyr	Gln	Pro	Ser	Gln	Glu	Phe	Ser	Phe	Thr	Ala	Thr	Phe	Glu	Val	Phe
			100					105					110		
Pro	Glu	Val	Glu	Leu	Lys	Gly	Leu	Glu	Asn	Ile	Glu	Val	Glu	Lys	Pro
	115						120					125			
Val	Val	Glu	Ile	Thr	Glu	Ala	Asp	Leu	Asp	Lys	Met	Ile	Asp	Val	Leu
	130					135					140				
Arg	Lys	Gln	Gln	Ala	Thr	Trp	Ala	Glu	Ser	Gln	Ala	Ala	Ala	Gln	Ala
145					150					155					160
Glu	Asp	Arg	Val	Val	Ile	Asp	Phe	Val	Gly	Ser	Val	Asp	Gly	Glu	Glu
			165						170					175	
Phe	Glu	Gly	Gly	Lys	Ala	Thr	Asp	Phe	Thr	Leu	Ala	Met	Gly	Gln	Ser
		180						185					190		
Arg	Met	Ile	Pro	Gly	Phe	Glu	Glu	Gly	Ile	Val	Gly	His	Lys	Ala	Gly
	195						200					205			
Glu	Gln	Phe	Asp	Ile	Asp	Val	Thr	Phe	Pro	Glu	Glu	Tyr	His	Ala	Glu
	210					215					220				
Asn	Leu	Lys	Gly	Lys	Ala	Ala	Lys	Phe	Ala	Ile	Thr	Leu	Lys	Lys	Val
225					230					235					240
Glu	Asn	Ile	Val	Leu	Pro	Glu	Leu	Thr	Glu	Glu	Phe	Val	Lys	Lys	Phe
			245						250					255	
Gly	Ser	Ala	Lys	Thr	Val	Glu	Asp	Leu	Arg	Ala	Glu	Ile	Lys	Lys	Asn
		260						265					270		
Met	Gln	Arg	Glu	Leu	Lys	Asn	Ala	Val	Thr	Ala	Arg	Val	Lys	Asn	Gln
	275						280					285			
Val	Ile	Asn	Gly	Leu	Ile	Ala	Gln	Asn	Glu	Ile	Glu	Val	Pro	Ala	Ala
	290					295					300				

Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
 305 310 315 320

Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
 325 330 335

Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
 340 345 350

Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
 355 360 365

Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
 370 375 380

Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
 385 390 395 400

Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
 405 410 415

Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
 420 425 430

Gly

<210> 162
 <211> 316
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> tRNA-glu

<400> 162
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 ggcctaggac atcgcccttt cacggcggtta accgggggttc gaatccccgt ggggacgccca 120
 tttaaagatg acttttggtg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180
 tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
 agctgaacaa aagcagctaa gtgtttagtt gaataaagta tcgcgttgaa tgcgttcaaa 300
 taaaatttga aaatat 316

<210> 163
 <211> 85
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> tRNA-leu

<400> 163
 gctctggtgg tggaattggt agacacgcta tcttgagggg gtagtgtcca taggatgtgc 60
 gagttcgagt ctgcccaga gcacc 85

<210> 164
 <211> 623
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> yaeE

<220>
 <221> CDS
 <222> (1) .. (621)

<400> 164
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 1 5 10 15
 ctt gaa acg ctc tat atg ggc ttt gcg gcg act tta ctt gct gtg gta 96
 Leu Glu Thr Leu Tyr Met Gly Phe Ala Thr Leu Leu Ala Val Val
 20 25 30
 gtc ggt ttg ccg atc ggt ttt ctg gca ttt tta acc ggt aaa gga gag 144
 Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
 35 40 45
 att tta gag aat ccg cgt tta cat caa gta tta gat gtg att att aat 192
 Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn
 50 55 60
 atc ggt cgt tcc gta ccg ttt att att ttg tta gtc gtg ttg tta cct 240
 Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro
 65 70 75 80
 ttt acg cgt tta ttg gtc ggg aca acg ctc ggt act acg gcg gcg att 288
 Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile
 85 90 95
 gtg ccg tta agc gtt tcg gca att ccg ttt ttt gcg cgt tta act tca 336
 Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser
 100 105 110
 aat gcg tta tta gaa atc cca gca ggt tta acc gaa gcg gcg aaa tcg 384
 Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser
 115 120 125
 atg ggc gca acg aat tgg caa gtg gtc agt aaa ttt tat tta ccg gaa 432
 Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu
 130 135 140
 tca ctg ccg att tta atc aat ggt atc aca tta act tta gtc gct tta 480
 Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu
 145 150 155 160
 atc ggt tat tcg gca atg gcg ggt gcg gtc ggc ggc ggc ggt ttg ggt 528
 Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly
 165 170 175
 aac ctt gcc atc agt tac ggt gaa cac cga aat atg gtc tat gta aaa 576
 Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys
 180 185 190
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<213> Actinobacillus pleuropneumoniae

<400> 165

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Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val
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Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
 35 40 45

Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn
 50 55 60

Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro
 65 70 75 80

Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile
 85 90 95

Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser
 100 105 110

Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser
 115 120 125

Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu
 130 135 140

Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu
 145 150 155 160

Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly
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Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys
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Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln
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His Phe Trp Tyr

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Asn Gln Asp Glu

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<400> 169

Ala Leu Ile Val Pro

1

5